

GenCore version 5.1.3
copyright (c) 1993 - 2003 Compugen Ltd.

Om protein - protein search, using sw model

Run on: January 17, 2003, 13:16:38 ; Search time 35 Seconds
(without alignments)

87,565 Million cell updates/sec

Title: US-09-641-034-47

Perfect score: 126

Sequence: 1 TDQERGNDISPFSGDQPFKD 23

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

~Geneseq_101002:*

1: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1980 DAT:*

2: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1981 DAT:*

3: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1982 DAT:*

4: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1983 DAT:*

5: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1984 DAT:*

6: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1985 DAT:*

7: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1986 DAT:*

8: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1987 DAT:*

9: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1988 DAT:*

10: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1989 DAT:*

11: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1990 DAT:*

12: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1991 DAT:*

13: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1992 DAT:*

14: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1993 DAT:*

15: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1994 DAT:*

16: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1995 DAT:*

17: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1996 DAT:*

18: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1997 DAT:*

19: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1998 DAT:*

20: /S1S2/gcdata/geneseq/geneseqp-emb1/AA1999 DAT:*

21: /S1S2/gcdata/geneseq/geneseqp-emb1/AA2000 DAT:*

22: /S1S2/gcdata/geneseq/geneseqp-emb1/AA2001 DAT:*

23: /S1S2/gcdata/geneseq/geneseqp-emb1/AA2002 DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	126	100.0	23 23	AAU33726
2	126	100.0	23 23	AAO20379
3	126	100.0	97 23	AAU33681
4	126	100.0	97 23	AAO20331
5	126	100.0	430 21	AYV53812
6	126	100.0	430 22	AAB2669
7	126	100.0	509 22	AAB2922
8	126	100.0	525 22	AAB2920
9	126	100.0	525 22	AAB2689
10	126	100.0	525 23	ABB08526

RESULT 1
ID AAU93726
XX AAU93726 standard; peptide; 23 AA.
AC AAU93726;
XX DT 02-JUL-2002 (first entry)
XX DE Dental product; bone growth enhancing peptide #46.
XX KW Dental product; toothpaste; mouthwash; dental floss; bone growth; KW integrin binding motif; RGD; skeletal disease; dental disease; tooth; KW alveolar bone growth; osteoblast; odontoblast; osteopathic.
OS Synthetic.
XX PN WO200213775-A1.
XX PD 21-FEB-2002.
XX PF 09-AUG-2001; 2001WO-US25101.
XX PR 16-AUG-2000; 2000US-225879P.
XX PA (BIGB-) BIG BMR BIO INC.
XX PI Yoneda T, Nomizu M, Kumagai Y;
XX WPI: 2002-329525/36.
XX PT Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif.
XX PT Human oncogenic os Human osteoregulin Human osteoregulin Human OOMI calcium Dental product bon Protein of matrix Human OOMI calcium C-terminal amide Dental product bon C-terminal amide Dental product bon Peptide of matrix Dental product bon C-terminal amide Dental product bon Peptide of matrix Protein of matrix Dental product bon Peptide of matrix Dental product bon Peptide of matrix Peptide of matrix Peptide of a calci Dental product bon Protein of matrix Dental product bon Protein of matrix Human bone marrow Human phospholipas Human porin peptid Rhodobacter capsul Sequence of porin Drosophila melanog Human OOMI calcium

XX
PS Claim 7; Page 21; 44pp; English.

CC The present invention relates to dental products such as toothpastes, CC mouthwash and dental floss comprising a base material and a compound CC which promotes bone growth. Such compounds are peptide sequences CC comprising 10-50 amino acids and containing an integrin binding CC motif such as RGD in the D- or L- form, preferably the L-configuration. CC The peptides of the invention are useful for treating or preventing CC skeletal diseases such as dental disease. The peptides enhance tooth CC and/or alveolar bone growth in areas where deterioration has occurred, CC as well as the growth or recruiting of osteoblast or odontoblast cells CC on the surface of the new skeletal growth. AAU93601-AAU93726 represent CC bone growth enhancing peptides for use in dental products.

XX Sequence 23 AA;

Query Match 100.0%; Score 126; DB 23; Length 23; Best Local Similarity 100.0%; Pred. No. 1.8e-12; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDLOQERGDNNDISPFGSGDQPKD 23
Db 1 TDLOQERGDNNDISPFGSGDQPKD 23

RESULT 2

AAO20379
ID AAO20379 standard; peptide: 23 AA.

XX
AC AAO20379;
XX
DT - 31-MAY-2002 (first entry)

XX
DE C-terminal amidated synthesised peptide D-00006.

XX
Bone growth; RGD motif; integrin binding motif; calcium binding motif; KW glycosaminoglycan binding motif; bone loss; renal phosphate excretion; KW alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; KW weakness; D00006.

XX
OS Synthetic.

XX
FH Key
FT Modified-site
FT 23
FT /note= "C-terminal amide"

XX
PN WO200213750-A1.

XX
PD 21-FEB-2002.

XX
PR 16-AUG-2000; 2000US-225879P.

XX
PR 09-APR-2001; 2001WO-US25101.

XX
PR 21-FEB-2002.

XX
PR 16-AUG-2000; 2000US-0641034.

XX
PR 19-MAR-2001; 2001US-0812485.

XX
PR 14-AUG-2001; 2001WO-US25542.

XX
PR WPI; 2002-291971/33.

XX
PS Example 1; Page 15; 50pp; English.

XX
CC The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful

CC for reducing bone loss and for reducing renal phosphate excretion in an CC individual. The peptide is useful for promoting regeneration of alveolar CC bone and/or teeth, and increases the number and activity of odontoblasts CC /osteoclasts that help form dental tissues. The peptide is also useful CC for treating or preventing a condition associated with skeletal loss or CC weakness. This sequence represents a C-terminal amidated synthesised CC peptide D-00006 of the invention.

XX Sequence 23 AA;

Query Match 100.0%; Score 126; DB 23; Length 23; Best Local Similarity 100.0%; Pred. No. 1.8e-12; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDLOQERGDNNDISPFGSGDQPKD 23
Db 1 TDLOQERGDNNDISPFGSGDQPKD 23

RESULT 3

AAU93681
ID AAU93681 standard; protein: 97 AA.

XX
AC AAU93681;

XX
DT 02-JUL-2002 (first entry)

XX
DE Dental product bone growth enhancing peptide #1.

XX
KW Dental product; toothpaste; mouthwash; dental floss; bone growth; KW intererin binding motif; RGD; skeletal disease; dental disease; tooth; KW alveolar bone growth; osteoblast; odontoblast; osteopathetic.

XX
OS Synthetic.

XX
PN WO200213755-A1.

XX
PD 21-FEB-2002.

XX
PR 16-AUG-2000; 2000US-225879P.

XX
PR 09-APR-2001; 2001WO-US25101.

XX
PR 21-FEB-2002.

XX
PR (BIG3-) BIG BEAR BIO INC.

XX
PI Yoneeda T, Nomizu M, Kumagai Y;

XX
DR WPI; 2002-329525/36.

XX
PR Dental product useful for treating skeletal diseases e.g. dental PR diseases comprises a base material and a compound comprising specific PR amino acid in a sequence containing the integrin binding motif.

XX
PS Disclosure; Page 11; 44pp; English.

XX
CC The present invention relates to dental products such as toothpastes, CC mouthwash and dental floss comprising a base material and a compound CC which promotes bone growth. Such compounds are peptide sequences CC comprising 10-50 amino acids and containing an integrin binding CC motif such as RGD in the D- or L- form, preferably the L-configuration. CC The peptides of the invention are useful for treating or preventing CC skeletal diseases such as dental disease. The peptides enhance tooth CC and/or alveolar bone growth in areas where deterioration has occurred, CC as well as the growth or recruiting of osteoblast or odontoblast cells CC on the surface of the new skeletal growth. AAU93601-AAU93726 represent CC bone growth enhancing peptides for use in dental products.

XX
PS Sequence 97 AA;

Query Match 100.0%; Score 126; DB 23; Length 97; Best Local Similarity 100.0%; Pred. No. 9.1e-12; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	TDLQERGDNNDISPPSGDGQPKD	23	DT	22-FEB-2000	(first entry)
Db	43	TDLQERGDNNDISPPSGDGQPKD	65	DE	Amino acid sequence of a human phosphatotin polypeptide.	
RESULT 4				KW	Human; phosphatotin; Metastatic-tumour Excreted Phosphaturic-Element;	
AA00331				KW	NEPE; Na ⁺ -dependent phosphate cotransport; vitamin D metabolism;	
ID AA020331	standard; protein; 97 AA.			KW	bone mineralisation; phosphate metabolism related disease;	
XX				KW	hyperphosphatemia; renal osteodystrophy; renal dialysis;	
AC AA020331;				KW	secondary hyperparathyroidism; osteitis fibrosa cystica; hypercalciuria;	
XX				KW	x-linked hypophosphatemic rickets; hereditary hypophosphatemic rickets;	
DT 31-MAY-2002	(first entry)			KW	hypomineralised bone lesion; stunted growth; cystic fibrosis;	
DE Protein of matrix extracellular phosphoglycoprotein containing RGD #1.				KW	oncogenic hypophosphatemic osteomalacia; renal phosphate leakage;	
XX				KW	renal osteodystrophy; osteoporosis; vitamin D resistant rickets;	
KW Bone growth; RGD motif; integrin binding motif; calcium binding motif;				KW	Paget's disease; kidney failure; renal tubular acidosis; sprue;	
KW alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;				XX	osmotic diuresis; renal Fanconi syndrome; autosomal rickets;	
KW weakness; matrix extracellular phosphoglycoprotein.				OS	Homo sapiens.	
XX Unidentified.				FH	Location/Qualifiers	
XX WO200213360-A1.				FT	Key	
PN				FT	Modified-site	8.10
XX				FT	Modified-site	/note= "protein kinase C phosphorylation site"
PD 21-FEB-2002.				FT	Modified-site	8.11
XX				FT	Modified-site	/note= "Casein kinase II phosphorylation site"
PF 14-AUG-2001; 2001WO-US25542.				FT	Modified-site	16.21
XX				FT	Modified-site	/note= "myristoylation site"
PR 16-AUG-2000; 2000US-0641034.				FT	Modified-site	40.47
PR 19-MAR-2001; 2001US-0812485.				FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
XX (BIGB-) BIG BEAR BIO INC.				FT	Modified-site	77..79
XX Kumagai Y, Blacher RW, Yoneda T;				FT	Modified-site	/note= "protein kinase C phosphorylation site"
PI DR XX				FT	Modified-site	118..120
PS WPI; 2002-291971/33.				FT	Modified-site	/note= "protein kinase C phosphorylation site"
PT New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprising an integrin binding motif, a glycosaminoglycan binding motif or a calcium binding motif.				FT	Modified-site	119..224
PT Disclosure; Page 11; 50pp; English.				FT	Modified-site	/note= "myristoylation site"
XX The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L-conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.				FT	Modified-site	139..142
XX Sequence 97 AA;				FT	Modified-site	/note= "Casein kinase II phosphorylation site"
Query Match 100.0%; score 126; DB 23; Length 97;				FT	Modified-site	145..148
Best Local Similarity 100.0%; Pred. No. 9.1e-12; Mismatches 0; Indels 0; Gaps 0;				FT	Modified-site	/note= "glycosaminoglycan attachment site"
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				FT	Region	177..180
Oy 1 TDLQERGDNNDISPPSGDGQPKD 23				FT	Modified-site	/note= "myristoylation site"
Db 43 TDLQERGDNNDISPPSGDGQPKD 65				FT	Modified-site	152..154
RESULT 5				FT	Modified-site	/note= "cell attachment tripeptide"
AY53812 standard; protein; 430 AA.				FT	Modified-site	161..165
ID AY53812				FT	Modified-site	/note= "glycosaminoglycan attachment site"
XX				FT	Modified-site	174..197
FT /note= "Casein kinase II phosphorylation site"				FT	Modified-site	198..202
FT /note= "Casein kinase II phosphorylation site"				FT	Modified-site	203..205
FT /note= "protein kinase C phosphorylation site"				FT	Modified-site	224..227
FT /note= "casein kinase II phosphorylation site"				FT	Modified-site	228..231
FT /note= "Casein kinase II phosphorylation site"				FT	Modified-site	228..230
FT /note= "protein kinase C phosphorylation site"				FT	Modified-site	238..241
FT /note= "Casson kinase II phosphorylation site"				FT	Modified-site	266..271
FT /note= "myristoylation site"				FT	Modified-site	291..296
FT /note= "myristoylation site"				FT	Modified-site	311..313
FT /note= "protein kinase C phosphorylation site"				FT	Modified-site	312..314
FT /note= "protein kinase C phosphorylation site"				FT	Modified-site	315..320
FT /note= "myristoylation site"				FT	Modified-site	319..321
FT /note= "protein kinase C phosphorylation site"				FT	Modified-site	325..328
FT /note= "Casein kinase II phosphorylation site"				FT	Modified-site	370..373
FT /note= "amidation site"				FT	Modified-site	

FT	Modified-site	382..386	QY	1	TDQERGDNDISPRSGDQPFKD 23
FT	Modified-site	/note= "Asu-glycosylation site"	Db	147	TDQERGDNDISPRSGDQPFKD 169
FT	Modified-site	/note= "Asu-glycosylation site"	ID	AAB62669	RESULT 6
FT	Modified-site	384..386	ID	AAB62669	standard; Protein; 430 AA
FT	Modified-site	/note= "protein kinase C phosphorylation site"	XX		
FT	Modified-site	389..394	XX		
FT	Modified-site	/note= "protein kinase C phosphorylation site"	XX		
FT	Modified-site	403..405	XX		
FT	Modified-site	/note= "protein kinase C phosphorylation site"	XX		
FT	Modified-site	405..408	XX		
FT	Modified-site	/note= "CAMP and cGMP dependent protein kinase phosphorylation site"	XX		
FT	Modified-site	408..410	XX		
FT	Modified-site	/note= "protein kinase C phosphorylation site"	XX		
FT	Modified-site	409..411	XX		
FT	Modified-site	/note= "protein kinase C phosphorylation site"	XX		
FT	Modified-site	423..426	XX		
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	XX		
FT	Modified-site	425..428	OS		
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	OS		
FT	Modified-site	427..430	OS		
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	OS		
XX	W0960017-A2.		XX		
PN			XX		
PD	25-NOV-1999.		XX		
XX			XX		
PF	18-MAY-1999;	99WO-EP03403.	XX		
XX			XX		
PR	18-MAY-1998;	98GB-0010681.	PD		
PR	04-SEP-1998;	98GB-0019387.	XX		
XX	(UNIL) UNIV COLLEGE LONDON.		PR		
PA	Rowe P;		XX		
PI			PR		
XX	WPI: 2000-051262/04.		XX		
DR	DR - N-PSDB; AAZ36447.		XX		
XX			XX		
PT	New polypeptides involved in the regulation of phosphate metabolism useful for diagnosing and treating disorders related to phosphate metabolism		XX		
PT	Claim 6; Fig 8; 13pp; English.		XX		
CC	The present sequence represents a phosphatotin polypeptide (also called Metastatic-tumour Excreted Phosphaturic-Element (MEPE)). The level of phosphatotin in a subject modulates Na+-dependent phosphate cotransport, vitamin D metabolism and/or bone mineralisation. The phosphatotin polypeptides, polynucleotides, vectors and antibodies are used to treat phosphate metabolism related disease. They are used for treatment of hyperphosphatemia, or renal osteodystrophy, hyperphosphatemia in renal dialysis/pre-dialysis, secondary hyperparathyroidism or osteitis fibrosa cystica, or X-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets with hypocalciuria (HHR), hypomineralised bone lesions, stunted growth in juveniles, oncogenic hypophosphatemic rickets, osteomalacia, renal phosphate leakage, renal osteodystrophy, renal osteoporosis, vitamin D resistant rickets, end organ resistance, renal Fanconi syndrome, cystic fibrosis or gout. It is used to prepare a medicament for treating X-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets with hypercalciuria (HHR), hypomineralized bone lesions, stunted growth in juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphate leakage, renal osteodystrophy, osteoporosis, vitamin D resistant rickets, end organ resistance, renal Fanconi syndrome, cystic fibrosis, Page's disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. Phosphatotin polynucleotides are useful as molecular weight markers on Southern gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatotin polypeptides are also useful for identifying agonists and antagonists, compounds which bind to phosphatotin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents a truncated form of phosphatotin (MEPE).		XX		
SQ	Sequence 430 AA;		XX		
Query Match	100.0%	Score 126; DB 21; Length 430;			
Best Local Similarity	100.0%	Pred. No. 5e-11; Mismatches 0; Indels 0; Gaps 0;			
Matches	23;	Conservative			
SQ	Sequence 430 AA;				

Query Match	100.0%	Score 126; DB 22;	Length 430;	Db	
Best Local Similarity	100.0%	Pred. No. 5e-11;	Length 509;	Db	
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	Db
Qy	1	TDIQLERGNDNDISPFSGDQCPFKD	23	TDIQLERGNDNDISPFSGDQCPFKD	248
Db	147	TDIQLERGNDNDISPFSGDQCPFKD	169	TDIQLERGNDNDISPFSGDQCPFKD	248
RESULT 7				RESULT 8	
AAB82922				AAB82920	
ID AAB82922	standard;	Protein;	509 AA.	ID AAB82920	standard;
XX				XX	
AC AAB82922;				AC AAB82920;	
XX				XX	
DT 21-DEC-2001	(first entry)			DT 21-DEC-2001	(first entry)
DE Human osteoregulin (mature polypeptide).				DE Human osteoregulin.	
XX				XX	
KW osteoregulin; human; bone; homeostasis; adipose; calcification; atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic; therapy.				KW osteoregulin; human; bone; homeostasis; adipose; calcification; atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic; therapy.	
XX				XX	
OS Homo sapiens.				OS Homo sapiens.	
XX				XX	
EP1130098-A2.				Key	Location/Qualifiers
XX				FT 1..37	/label= Signal_peptide
PD 05-SEP-2001.				FT 38..525	/label= Mature_protein
XX				PN EP1130098-A2.	
PF 27-FEB-2001; 2001EP-0301768.				PD 05-SEP-2001.	
XX				XX	
PR 29-FEB-2000; 2000US-185617P.				PR 27-FEB-2001; 2001EP-0301768.	
XX				XX	
PR 22-SEP-2000; 2000US-234500P.				PR 29-FEB-2000; 2000US-185617P.	
XX				PR 22-SEP-2000; 2000US-234500P.	
PA (PFIZ) PFIZER PROD INC.				PA (PFIZ) PFIZER PROD INC.	
XX				PI Brown TA, De Wet JR, Gowen LC, Hames LM;	
PT Brown TA, De Wet JR, Gowen LC, Hames LM;				XX	
XX DR N-PSDB; AAH26810.				DR N-PSDB; AAH26810.	
PT Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin.				XX	
PT PS Claim 1; Page 54-55; 90pp; English.				PT Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin.	
XX				PT PS Claim 1; Page 45-47; 90pp; English.	
CC The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence.				XX	
CC Osteoregulin is a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques.				CC The present sequence is that of human osteoregulin, a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques.	
CC were identified (see also AAB82923). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, or vascular flexibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.				CC The sequence is predicted from the nucleotide sequence (see AAH26808) of isolated osteoblast cDNA. A splice variant of human osteoregulin was also identified (see AAB8221). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.	
CC sequence 509 AA;				CC sequence 525 AA;	
SQ Query Match 100.0%; Score 126; DB 22; Length 509; Best Local Similarity 100.0%; Pred. No. 6.1e-11; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Query Match 100.0%; Score 126; DB 22; Length 525; Best Local Similarity 100.0%; Pred. No. 6.3e-11; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 TDLOLRGNDNDISPFSGDQCPFKD				Qy 1 TDLOLRGNDNDISPFSGDQCPFKD	

RESULT 15
 ID AAO20353 standard; protein: 40 AA.
 XX
 AC AAO20353;
 XX
 DT 31-MAY-2002 (first entry)
 DE Protein of matrix extracellular phosphoglycoprotein containing RGD #23.
 XX
 KW Bone growth; RGD motif; integrin binding motif; calcium binding motif;
 glycosaminoglycan binding motif; bone loss; renal phosphate excretion;
 alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
 weakness; matrix extracellular phosphoglycoprotein.
 XX
 OS Unidentified.
 XX
 PN WO200214360-A1.
 XX
 PD 21-FEB-2002.
 XX
 PP 14-AUG-2001; 2001WO-US25542.
 XX
 PR 16-AUG-2000; 2000US-0641034.
 PR 19-MAR-2001; 2001US-0812485.
 XX
 PA (BIGB-) BIG BEAR BIO INC..
 XX
 PI Kumagai Y, Blacher RW, Yoneda T;
 XX
 DR WPI: 2002-291971/33.
 XX
 PT New peptide compound useful for reducing bone loss, is capable of
 enhancing bone growth, and comprises an integrin binding motif,
 glycosaminoglycan binding motif or a calcium binding motif.
 XX
 PS Disclosure; Page 12; 50pp; English.
 XX
 CC The invention relates to a peptide compound capable of enhancing bone
 growth, and comprising 10-50 amino acids in a sequence, where the amino
 acids are in D- or L- conformation and the sequence comprises a motif
 selected from an integrin binding motif, a glycosaminoglycan binding
 motif and a calcium binding motif. The peptide of the invention is useful
 for reducing bone loss and for reducing renal phosphate excretion in an
 individual. The peptide is useful for promoting regeneration of alveolar
 bone and/or teeth, and increases the number and activity of odontoblasts
 /osteoclasts that help form dental tissues. The peptide is also useful
 for treating or preventing a condition associated with skeletal loss or
 weakness. This sequence represents a protein of a matrix extracellular
 phosphoglycoprotein containing an RGD motif of the invention.
 XX
 Sequence 40 AA:

Query Match 80.2%; Score 101; DB 23; Length 40;
 Best Local Similarity 100.0%; Pkd. No. 2.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RGNDISFSGDGQPFK 23
 Db 1 RGNDISFSGDGQPFK 18

Search completed: January 17, 2003, 13:17:44
 Job time : 36 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

On Protein - protein search, using sw model

Run on: January 17, 2003, 13:16:42 ; Search time 14 Seconds
(without alignments)
49.338 Million cell updates/sec

Title: US-09-641-034-47
Perfect score: 126
Sequence: 1 TDQERGDDNDISPFSSGQPFKD 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA-*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/1aa/pcrus_COMB.pep:
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

RESULT 1
US-08-355-844-2
; Sequence 2, Application US/08355844
; Patent No. 5340307

GENERAL INFORMATION:

APPLICANT: Fischbarg, Jorge
APPLICANT: Czegledy, Ferenc
APPLICANT: Iserovich, Pavel
APPLICANT: Li, Jun
APPLICANT: Cheung, Min

TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,844
FILING DATE: 14-DEC-1994

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.

REGISTRATION NUMBER: 29,705

REFERENCE/DOCKET NUMBER: A29927-50/29910

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..301
OTHER INFORMATION: Porin protein

US-08-355-844-2

28 42.5 33.7 306 1 US-08-474-042-1
29 42.5 33.7 306 1 US-08-484-558-1
30 42.5 33.7 306 1 US-08-574-593-1
31 42.5 33.7 448 1 US-08-295-411-3
32 42.5 33.7 448 2 US-08-955-471-3
33 42.5 33.7 448 5 PCM-US93-10068-1
34 42.5 33.7 448 5 PCM-US93-10242-3
35 42.5 33.7 488 1 US-08-487-037-1
36 42.5 33.7 545 2 US-08-990-114-1
37 42.5 33.7 545 4 US-09-241-333-1
38 41.5 32.9 364 4 US-08-858-207A-313
39 41.5 32.9 811 4 US-08-983-275-2
40 40.5 32.1 397 4 US-09-087-134-17
41 40 31.7 469 2 US-08-416-870C-6
42 40 31.7 795 4 US-09-370-807-6
43 40 31.7 795 4 US-09-921-559-6
44 40 31.7 831 2 US-09-047-026A-4
45 40 31.7 912 5 PCM-US93-03747-2

ALIGNMENTS

Query Match 41.3%; Score 52; DB 2; Length 301;
 Best Local Similarity 58.8%; Pred. No. 2.8; 2; Mismatches
 Matches 10; Conservative 5; Indels 0; Gaps 0;

RESULT 2
 PCT-US95-16126-2
 ; Sequence 2, Application PC/TUS9516126
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischberg, Jorge
 ; APPLICANT: Czagledy, Ferenc
 ; APPLICANT: Isetrovich, Pavel
 ; APPLICANT: Li, Jun
 ; APPLICANT: Cheung, Min
 ; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10112-0228
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/16126
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/355,844
 ; FILING DATE: 14-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tang, Henry Y.S.
 ; REGISTRATION NUMBER: 29,705
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-408-2586
 ; TELEFAX: 212-765-2519
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 301 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..301
 ; OTHER INFORMATION: Porin protein
 ; PCT-US95-16126-2

Query Match 41.3%; Score 52; DB 5; Length 301;
 Best Local Similarity 53.8%; Pred. No. 2.8; 2; Mismatches
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 3
 ; Sequence 3, Application PC/TUS9516126
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GIC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3614
 ; LENGTH: 815
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3614

Query Match 37.3%; Score 47; DB 4; Length 815;
 Best Local Similarity 58.8%; Pred. No. 50; 0; Mismatches
 Matches 10; Conservative 0; Indels 0; Gaps 0;

RESULT 4
 US-09-199-637A-405
 ; Sequence 405, Application US/09199637A
 ; Patent No. 6355411
 ; GENERAL INFORMATION:
 ; APPLICANT: Ausubel, Frederick
 ; APPLICANT: Goodman, Howard M.
 ; APPLICANT: Rahme, Laurence G.
 ; APPLICANT: Mahajan-Miklos, Shalina
 ; APPLICANT: Tan, Man-Wah
 ; APPLICANT: Cao, Hui
 ; APPLICANT: Drenkard, Eliana
 ; APPLICANT: Tsongalis, John
 ; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
 ; FILE REFERENCE: 00716/361002
 ; CURRENT APPLICATION NUMBER: US/09/199,637A
 ; CURRENT FILING DATE: 1998-11-25
 ; PRIOR APPLICATION NUMBER: 60/066,517
 ; PRIOR FILING DATE: 1997-11-25
 ; NUMBER OF SEQ ID NOS: 437
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 405
 ; LENGTH: 1198
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-199-637A-405

Query Match 37.3%; Score 47; DB 4; Length 1198;
 Best Local Similarity 52.4%; Pred. No. 77; 4; Mismatches
 Matches 11; Conservative 2; Indels 4; Gaps 1;

RESULT 5
 US 08-341-843B-9
 ; Sequence 9, Application US/08341843B
 ; Patent No. 587225
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemmon, Vance

TITLE OF INVENTION: A Method for Characterizing the Nucleotide Sequence of LICAM and
 TITLE OF INVENTION: Nucleotide Sequence of LICAM and
 Patent No. 5872225
 TITLE OF INVENTION: the Nucleotide Sequence
 TITLE OF INVENTION: Characterized Thereby
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fay, Sharpe, Beall, Fagan,
 STREET: Suite 700
 CITY: Cleveland
 STATE: Ohio
 COUNTRY: U.S.A.
 ZIP: 44114-2518
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 MEDIUM TYPE: storabile
 COMPUTER: Compaq Prolinea 5100e
 OPERATING SYSTEM: DOS 5.0
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/341,843B
 FILING DATE: No. 5872225ember 18, 1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/904,991
 ATTORNEY/AGENT INFORMATION:
 NAME: Minich, Richard J.
 REGISTRATION NUMBER: 24,175
 REFERENCE/DOCKET NUMBER: CWR 2 149-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (216) 861-5582
 TELEFAX: (216) 241-1666
 TELEX: (216) 980162
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: amino acids
 HYPOTHETICAL: irrelevant
 ANTI-SENSE: no
 ORIGINAL SOURCE:
 ORGANISM: mouse
 INDIVIDUAL ISOLATE: 8 day old mouse brain
 IMMEDIATE SOURCE:
 LIBRARY: lambda GT 10 and lambda GT11
 CLONE: synthesis of several clones
 PUBLICATION INFORMATION:
 AUTHORS: Moos, M.
 AUTHORS: Tacke, R.
 AUTHORS: Scherer, H.
 AUTHORS: Teplow, D.
 AUTHORS: Fruh, K.
 AUTHORS: Schachner, M.
 TITLE: Neural adhesion molecule L1 is a member of the immunoglobulin superfamily with binding domains
 TITLE: similar to fibronectin
 JOURNAL: NATURE
 VOLUME: 334
 ISSUE: 334
 PAGES: 701-703
 DATE: 1988
 US-08-341-843B-9

Query Match 36.1%; Score 45.5; DB 2; Length 96;
 Best Local Similarity 61.1%; Pred. No. 7.3;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 DQOERGDNNDTSPFGDQ 19
 RESULT 5
 US-08-427-497E-14
 ; Sequence 14, Application US/08427497E
 ; Patent No. 5969124
 ; Db 41 DQERGDSO-KYFFEDGK 57

QY 2 DQOERGDNNDTSPFGDQ 19
 RESULT 5
 US-08-427-497E-14
 ; Sequence 14, Application US/08427497E
 ; Patent No. 5969124
 ; General Information:
 ; APPLICANT: Lemmon, Vance
 ; TITLE OF INVENTION: A Method for Characterizing the Nucleotide Sequence of LICAM and
 ; TITLE OF INVENTION: Nucleotide Sequence of LICAM and
 ; Patent No. 5969124
 ; TITLE OF INVENTION: the Nucleotide Sequence
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
 ; STREET: 1100 Superior Avenue
 ; CITY: Cleveland
 ; STATE: Ohio
 ; COUNTRY: U.S.A.
 ; ZIP: 44114-2518
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 ; MEDIUM TYPE: storabile
 ; COMPUTER: Compaq Prolinea 5100e
 ; OPERATING SYSTEM: DOS 5.0
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/427,497E
 ; FILING DATE: April 24, 1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/904,991
 ; FILING DATE: June 26, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Minich, Richard J.
 ; REGISTRATION NUMBER: 24,175
 ; REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
 ; TELEPHONE: (216) 861-5582
 ; TELEFAX: (216) 241-1666
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 96
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: amino acids
 ; HYPOTHETICAL: irrelevant
 ; ANTI-SENSE: no
 ; ORIGINAL SOURCE:
 ; ORGANISM: mouse
 ; INDIVIDUAL ISOLATE: 8 day old mouse brain
 ; IMMEDIATE SOURCE:
 ; LIBRARY: lambda GT 10 and lambda GT11
 ; CLONE: synthesis of several clones
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Moos, M.
 ; AUTHORS: Tacke, R.
 ; AUTHORS: Scherer, H.
 ; AUTHORS: Teplow, D.
 ; AUTHORS: Fruh, K.
 ; AUTHORS: Schachner, M.
 ; TITLE: Neural adhesion molecule L1 is a member of the immunoglobulin superfamily with binding domains
 ; TITLE: similar to fibronectin
 ; JOURNAL: NATURE
 ; VOLUME: 334
 ; ISSUE: 334
 ; PAGES: 701-703
 ; DATE: 1988
 ; US-08-341-843B-9

Query Match 36.1%; Score 45.5; DB 2; Length 96;
 Best Local Similarity 61.1%; Pred. No. 7.3;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

JOURNAL: NATURE
 VOLUME: 334
 ISSUE: 701-703
 PAGES: 1988
 DATE: 1988
 US-08-427-497E-14

Query Match 36.1%; Score 45.5; DB 2; Length 96;
 Best Local Similarity 61.1%; Pred. No. 7.3; 2; Mismatches
 Matches 11; Conservative 2; Indels 4; Gaps 1;
 QY 2 DQERGNDNDISPPSGDQ 19
 Db 41 DQERGSD-KYFIEDGK 57

RESULT 7
 US-08-506-296B-21

; Sequence 21, Application US/08506296B
 ; Patent No. 631265

GENERAL INFORMATION:
 APPLICANT: Phillips, Greg

APPLICANT: Cunningham, Bruce A.

APPLICANT: Crossin, Kathryn L.

TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
 TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE

NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute

STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTY: U.S.
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/506,296B

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/506,296B

APPLICATION NUMBER: US/08/506,296B
 FILING DATE: 24-JUL-1995
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Fietting, Thomas
 REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 488.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312

INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1260 amino acids

SEQUENCE: CHARACTERISTICS:
 LENGTH: 1260 amino acids

TYPE: amino acid
 TOPology: linear
 MOLECULE TYPE: protein

RESULT 8
 US-08-176-12B-2

Query Match 34.9%; Score 44; DB 1; Length 348;

Best Local Similarity 53.3%; Pred. No. 53; 3; Mismatches
 Matches 8; Conservative 4; Indels 0; Gaps 0;

QY 1 TDQERGNDNDISFS 15
 Db 320 TELOQETDNEMEPRS 334

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/669,435

APPLICATION NUMBER: US/08/669,435
 FILING DATE: 26-JUN-1995
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,126
 FILING DATE: 29-DEC-1993
 CLASSIFICATION:

RESULT 9
 US-08-669-435-2
 ; Sequence 2, Application US/08669435
 ; Patent No. 5869365
 GENERAL INFORMATION:
 APPLICANT: Dawson, Paul A.
 APPLICANT: Dawson, Paul A.
 TITLE OF INVENTION: IILEAL BILE ACID TRANSPORTER COMPOSITIONS AND
 TITLE OF INVENTION: METHODS
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: US
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,435
 FILING DATE: 26-JUN-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,126
 FILING DATE: 29-DEC-1993
 CLASSIFICATION:
 ; APPLICANT: Dawson, Paul A.

RESULT 8

Query Match 36.1%; Score 45.5; DB 4; Length 1260;

Best Local Similarity 61.1%; Pred. No. 1.4e+02; 2; Mismatches
 Matches 11; Conservative 2; Indels 1; Gaps 1;

QY 2 DQERGNDNDISPSGDDQ 19
 Db 558 DQERGSD-KYFIEDGK 574

RESULT 8

Query Match 36.1%; Score 45.5; DB 4; Length 1260;

Best Local Similarity 61.1%; Pred. No. 1.4e+02; 2; Mismatches
 Matches 11; Conservative 2; Indels 1; Gaps 1;

QY 2 DQERGNDNDISPSGDDQ 19
 Db 558 DQERGSD-KYFIEDGK 574

RESULT 8

Query Match 36.1%; Score 45.5; DB 4; Length 1260;

Best Local Similarity 61.1%; Pred. No. 1.4e+02; 2; Mismatches
 Matches 11; Conservative 2; Indels 1; Gaps 1;

QY 2 DQERGNDNDISPSGDDQ 19
 Db 558 DQERGSD-KYFIEDGK 574

ATTORNEY/AGENT INFORMATION:
 NAME: Parker, David L.
 REGISTRATION NUMBER: 332,165
 REFERENCE/DOCKET NUMBER: WAKE:002/PAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEX: (512) 471-7577
 FAX: (512) 471-7577
 ;
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 348 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08 669 435-2

RESULT 10
 PCT-US94-14431A-2
 Sequence 2, Application PC/US9414431A
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P. O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14431A
 FILING DATE: 29-DEC-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: PARKER, DAVID L.
 REGISTRATION NUMBER: 332,165
 REFERENCE/DOCKET NUMBER: WAKE0005P-
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEX: (713) 789-2679
 FAX: (713) 789-2679
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 348 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US94-14431A-2

Query Match 34.9%; Score 44; DB 5; Length 348;
 Best Local Similarity 53.3%; Pred. No. 53;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
 US-08-278-091-6
 Sequence 6, Application US/08278091
 Patent No. 5506139
 GENERAL INFORMATION:
 APPLICANT: LOOSMORE, Sheena M.
 APPLICANT: YANG, Yan-Ping
 APPLICANT: CHONG, Pele
 APPLICANT: OOMEN, Raymond P.
 APPLICANT: KLEIN, Michel H.
 TITLE OF INVENTION: Analog of Haemophilus Htr47 Protein with Reduced Protease Activity
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: Suite 701, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: MSG 1R7
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/278,091
 FILING DATE: 21-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Stewart, Michael I.
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-371
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEX: (416) 55-1163
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-08-278-091-6

RESULT 12
 US-08-483-859-6
 Sequence 6, Application US/08483859
 Patent No. 5656436
 GENERAL INFORMATION:
 APPLICANT: LOOSMORE, Sheena M.
 APPLICANT: YANG, Yan-Ping
 APPLICANT: CHONG, Pele
 APPLICANT: OOMEN, Raymond P.
 APPLICANT: KLEIN, Michel H.
 TITLE OF INVENTION: Analog of Haemophilus Htr47 Protein with Reduced Protease Activity
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/296,149
 FILING DATE: 26-AUG-1994
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/278,091
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I.
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-493 MIS:vg
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

08-472-173-6

RESULT 14

Query Match	Score	DB	Length	1;	Pred.	No.	Length	475;
Sequence 2, Application US/08350741	34.9%	2;	Mismatches	4;	Indels	0;	Gaps	0;
Patent No. 5804194	57.1%							

GENERAL INFORMATION:

APPLICANT: DOUGAN G.,
 APPLICANT: HORMAECHE C. E.,
 APPLICANT: CHARLES I.G.,
 APPLICANT: JOHNSON K.S.,
 APPLICANT: CHATFIELD S.N.

TITLE OF INVENTION: LIVE VACCINES

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON and VANDERHVE PC
 STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/350,741
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,737
 FILING DATE: 09-MAY-1994
 APPLICATION NUMBER: US 07/952,737
 FILING DATE: 30-NOV-1992
 APPLICATION NUMBER: GB 9007194.5
 FILING DATE: 30-MAR-1990
 APPLICATION NUMBER: PCT/GB91/00484
 FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
 REGISTRATION NUMBER: 32,955
 REFERENCE/DOCKET NUMBER: 117-158
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100
 TELEX: 200797 NJXN UR
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-350-741-2

Query Match

Best Local Similarity 34.9%; Score 44; DB 2; Length 475;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 10 DISPPSGDQPFKD 23

Db 79 DDSPPCQDQSPFQN 92

Search completed: January 17, 2003, 13:18:59

Job time : 15 secs

RESULT 15

US-08-487-167-6
 Sequence 6, Application US/08487167

PATENT NO. 5863102
 GENERAL INFORMATION:
 APPLICANT: LOOSHORE, Sheena M.
 APPLICANT: YANG, Yan-Ping
 APPLICANT: CHONG, Pele
 APPLICANT: OOMEN, Raymond P.

APPLICANT: KLEIN, Michel H.
 TITLE OF INVENTION: Analog of Haemophilus Hn47 Protein with
 NUMBER OF SEQUENCES: 23
 NUMBER OF INVENTION: Reduced Protease Activity
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: Suite 701, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: MSG 1R7

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,167
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/296,149
 FILING DATE: 26-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,091
 FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Stewart, Michael I.
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-508 MSS:vg
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-487-167-6

Query Match 34.9%; Score 44; DB 2; Length 475;
 Best Local Similarity 57.1%; Pred. No. 76;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 13:18:07 ; Search time 10 Seconds

(without alignments) 45.721 Million cell updates/sec

Title: US-09-641-034-47

Perfect score: 126

Sequence: TDLOERGDNDISPFSGDGQPFKD 23

Scoring table: Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pupbaa/us08_NEW_PUB.pep: *
2: /cgn2_6/ptodata/1/pupbaa/PC1_NEW_PUB.pep: *
3: /cgn2_6/ptodata/1/pupbaa/us06_NEW_PUB.pep: *
4: /cgn2_6/ptodata/1/pupbaa/us05_PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pupbaa/us07_PUBCOMB.pep: *
6: /cgn2_6/ptodata/1/pupbaa/us08_PUBCOMB.pep: *
7: /cgn2_6/ptodata/1/pupbaa/us09_PUBCOMB.pep: *
8: /cgn2_6/ptodata/1/pupbaa/us08_PUBCOMB.pep: *
9: /cgn2_6/ptodata/1/pupbaa/us09_NEW_PUB.pep: *
10: /cgn2_6/ptodata/1/pupbaa/us09_PUBCOMB.pep: *
11: /cgn2_6/ptodata/1/pupbaa/us10_NEW_PUB.pep: *
12: /cgn2_6/ptodata/1/pupbaa/us10_PUBCOMB.pep: *
13: /cgn2_6/ptodata/1/pupbaa/us60_NEW_PUB.pep: *
14: /cgn2_6/ptodata/1/pupbaa/us60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	126	100.0	23	9	US-09-812-485A-49
2	126	100.0	97	9	US-09-812-485A-1
3	126	100.0	525	10	US-09-814-550-2
4	101	80.2	40	9	US-09-812-485A-23
5	86	68.3	19	10	US-09-814-550-6
6	84	66.7	15	9	US-09-812-485A-48
7	84	66.7	33	9	US-09-812-485A-30
8	82	65.1	15	9	US-09-812-485A-47
9	59.5	15	9	US-09-812-485A-46	
10	73.5	58.3	40	9	US-09-812-485A-24
11	72.5	57.5	30	9	US-09-812-485A-26
12	72.5	35	12	9	US-09-812-485A-25
13	52.4	62.0	9	9	US-09-812-485A-42
14	57	45.2	40	9	US-09-812-485A-32
15	57	45.2	32	9	US-09-812-485A-27
16	53	42.1	45	9	US-09-812-485A-27
17	52	41.3	1458	12	US-10-054-691-2
18	52	41.3	19	10	US-09-814-550-5
19	38.9	301	10	10	US-09-905-176-23

ALIGNMENTS

RESULT 1

US-09-812-485A-49
Sequence 49, Application US-09812485A
Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshihara

APPLICANT: Blacher, Russell

APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing

TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases

FILE REFERENCE: BEAM-005CIP

CURRENT APPLICATION NUMBER: US/09/812,485A

PRIOR APPLICATION NUMBER: 09/641,034

PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 49

LENGTH: 23

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: D-00006 Peptide

NAME/KEY: AMIDATION

LOCATION: 15

US-09-812-485A-49

Query Match Best Local Similarity 100.0%; Pred. No. 5.2e-13;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

US-09-812-485A-1

Sequence 1, Application US/09812485A

Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshihara

APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki
 TITLE OF INVENTION: Integrin Binding Motif Containing Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 PRIORITY FILING DATE: 2001-03-19
 PRIORITY APPLICATION NUMBER: 09/641,034
 CURRENT FILING DATE: 2001-03-19
 PRIORITY FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 97
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: peptidic compound
 US-09-812-485A-1

Query Match 100.0%; Score 126; DB 9; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2 6e-12; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDQERGNDNDSPFSGDGQPKD 23
 Db 43 TDQERGNDNDSPFSGDGQPKD 65

RESULT 3
 US-09-814-550-2
 Sequence 2, Application US/09814550
 Patent No. US20020105641A1

GENERAL INFORMATION:
 APPLICANT: Schiavi, Susan
 APPLICANT: Madden, Stephen
 APPLICANT: Manavalan, Parthasarathy
 APPLICANT: Levine, Michael
 APPLICANT: Jan de Beur, Suzanne

FILE REFERENCE: 5014US
 CURRENT APPLICATION NUMBER: US/09/814,550
 CURRENT FILING DATE: 2001-03-22
 PRIORITY FILING DATE: 2000-03-24
 PRIORITY APPLICATION NUMBER: US 60/191,786
 PRIORITY FILING DATE: 2000-03-24
 PRIORITY APPLICATION NUMBER: US 60/241,598
 PRIORITY FILING DATE: 2000-10-19
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 2
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-814-550-2

Query Match 100.0%; Score 126; DB 10; Length 525;
 Best Local Similarity 100.0%; Pred. No. 1 8e-11; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDQERGNDNDSPFSGDGQPKD 23
 Db 242 TDQERGNDNDSPFSGDGQPKD 264

RESULT 4
 US-09-812-485A-23
 Sequence 23, Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIORITY FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 97
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: peptidic compound
 US-09-812-485A-1

Query Match 100.0%; Score 126; DB 9; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2 6e-12; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDQERGNDNDSPFSGDGQPKD 23
 Db 43 TDQERGNDNDSPFSGDGQPKD 65

RESULT 5
 US-09-814-550-6
 Sequence 6, Application US/09814550
 Patent No. US20020105641A1

GENERAL INFORMATION:
 APPLICANT: Schiavi, Susan
 APPLICANT: Madden, Stephen
 APPLICANT: Manavalan, Parthasarathy
 APPLICANT: Levine, Michael
 APPLICANT: Jan de Beur, Suzanne

FILE REFERENCE: 5014US
 CURRENT APPLICATION NUMBER: US/09/814,550
 CURRENT FILING DATE: 2001-03-22
 PRIORITY FILING DATE: 2000-03-24
 PRIORITY APPLICATION NUMBER: US 60/191,786
 PRIORITY FILING DATE: 2000-10-19
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 6
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-814-550-6

Query Match 80.2%; Score 101; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5 6e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RGNDNDSPFSGDGQPKD 23
 Db 1 RGNDNDSPFSGDGQPKD 18

RESULT 6
 US-09-812-485A-48
 Sequence 48, Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIORITY FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 97
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: peptidic compound
 US-09-812-485A-23

PRIOR FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 48
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: D-00005 peptide.
 NAME/KEY: AMIDATION
 LOCATION: 15
 US-09-812-485A-48

Query Match 66.7%; Score 84; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 NDISPFGDQPFKD 23
 Db 1 NDISPFGDQPFKD 15

RESULT 7
 US 09-812-485A-30
 Sequence 30, Application US/09812485A
 Publication No. US20020197267A1
 GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: 09/641,034
 PRIOR FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 30
 LENGTH: 33
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptidic compound
 US-09-812-485A-30

Query Match 66.7%; Score 84; DB 9; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 NDISPFGDQPFKD 23
 Db 1 NDISPFGDQPFKD 15

RESULT 8
 US-09-812-485A-47
 Sequence 47, Application US/09812485A
 Publication No. US20020197267A1
 GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: 09/641,034
 PRIOR FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 24

RESULT 9
 US-09-812-485A-46
 Sequence 46, Application US/09812485A
 Publication No. US20020197267A1
 GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: 09/641,034
 PRIOR FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 46
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: D-00003 peptide
 NAME/KEY: AMIDATION
 LOCATION: 15
 US-09-812-485A-46

RESULT 10
 US-09-812-485A-24
 Sequence 24, Application US/09812485A
 Publication No. US20020197267A1
 GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 FILE REFERENCE: BEAR-006CIP
 CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: 09/641,034
 PRIOR FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 24

US-09-812-485A-25

LENGTH: 40
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: peptidic compound
 OTHER INFORMATION: peptidic compound

US-09-812-485A-24

Query Match 58.3%; Score 73.5; DB 9; Length 40;
 Best Local Similarity 83.3%; Pred. No. 7.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 6 RCDNDISPFSGDQPFKD 23
 Db 4 RGB---SPFSGDQPFKD 18

RESULT 11
 US-09-812-485A-26
 Publication No. US20020197267A1

GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshihiko
 APPLICANT: Blacher, Russel
 APPLICANT: Yoneda, Toshiyuki
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

FILE REFERENCE:

BEAR-006CIP

CURRENT FILING DATE:

2001-03-19

PRIORITY NUMBER:

09/641,034

PRIOR FILING DATE:

2000-08-16

NUMBER OF SEQ ID NOS:

50

SOFTWARE:

FastSEQ for Windows Version 4.0

SEQ ID NO:

26

LENGTH:

30

TYPE: PRT

ORGANISM:

Artificial Sequence

FEATURE:

peptidic compound

OTHER INFORMATION:

peptidic compound

US-09-812-485A-42

Query Match 57.5%; Score 72.5; DB 9; Length 35;
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 9 NDISPPF---SGDQPFKD 23
 Db 1 NDISPFRGDQGQPFKD 18

RESULT 13

US-09-812-485A-42
 Sequence 42; Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshihiko

APPLICANT: Blacher, Russel

APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

FILE REFERENCE:

BEAR-006CIP

CURRENT FILING DATE:

2001-03-19

PRIORITY NUMBER:

09/641,034

PRIOR FILING DATE:

2000-08-16

NUMBER OF SEQ ID NOS:

50

SOFTWARE:

FastSEQ for Windows Version 4.0

SEQ ID NO:

42

LENGTH:

12

TYPE: PRT

ORGANISM:

Artificial Sequence

FEATURE:

peptidic compound

OTHER INFORMATION:

peptidic compound

US-09-812-485A-42

Query Match 52.4%; Score 66; DB 9; Length 12;
 Best Local Similarity 10.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DNDISPFSGDQ 19
 Db 1 DNDISPFSGDQ 12

RESULT 14

US-09-812-485A-32
 Sequence 32; Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshihiko

APPLICANT: Blacher, Russel

APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

FILE REFERENCE:

BEAR-006CIP

CURRENT FILING DATE:

2001-03-19

PRIORITY NUMBER:

09/641,034

PRIOR FILING DATE:

2000-08-16

NUMBER OF SEQ ID NOS:

50

SOFTWARE:

FastSEQ for Windows Version 4.0

SEQ ID NO:

32

LENGTH:

40

TYPE: PRT

ORGANISM:

Artificial Sequence

FEATURE:

peptidic compound

OTHER INFORMATION:

peptidic compound

US-09-812-485A-32

Query Match 45.2%; Score 57; DB 9; Length 40;
 Best Local Similarity 10.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NDISPFSGDQGQPFKD 23
 Db 1 NDISPFRGDQGQPFKD 18

RESULT 11

US-09-812-485A-26
 Sequence 26; Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshihiko

APPLICANT: Blacher, Russel

APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

FILE REFERENCE:

BEAR-006CIP

CURRENT FILING DATE:

2001-03-19

PRIORITY NUMBER:

09/641,034

PRIOR FILING DATE:

2000-08-16

NUMBER OF SEQ ID NOS:

50

SOFTWARE:

FastSEQ for Windows Version 4.0

SEQ ID NO:

35

LENGTH:

30

TYPE: PRT

ORGANISM:

Artificial Sequence

FEATURE:

peptidic compound

OTHER INFORMATION:

peptidic compound

Qy 14 FSGDQOPFKD 23
|||||||
1 FSGDQOPFKD 10

RESULT 15
US-09-812-485A-27
; Sequence 27, Application US/09812485A
; Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Koshiyuki
APPLICANT: Blcher, Russell

APPLICANT: Yoneida, Roshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A

CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/641,034

PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50

SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 27

LENGTH: 45

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: peptidic compound
US-09-812-485A-27

Query Match 45.2%; Score 57; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.027; DB 9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 FSGDQOPFKD 23
|||||||
1 FSGDQOPFKD 10

Search completed: January 17, 2003, 13:22:03
Job time : 10 secs

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 17, 2003, 13:17:52 ; Search time 15 Seconds
(without alignments) 112.414 Million Cell updates/sec

Title: US-09-641-034-47

Perfect score: 126

Sequence: 1 TDLOERGNDNDISPFGSGDQPKD 23

Scoring table: BLOSUM62

Gpop 10.0 , Gapext 0.5

Searched: 273288 seqs, 73313625 residues

Total number of hits satisfying chosen parameters: 273288

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query	Match	Length	DB	ID	Description
1	47	37.3	815	6	US-10-092-411A-3614		Sequence 3614, AP
2	46.5	36.9	1141	6	US-10-143-087A-437		Sequence 437, APP
3	46.5	36.9	1141	6	US-10-143-031A-437		Sequence 437, APP
4	46.5	36.9	1141	6	US-10-143-092A-437		Sequence 437, APP
5	46.5	36.9	1141	6	US-10-162-522A-437		Sequence 437, APP
6	46.5	36.9	1141	6	US-10-165-038A-437		Sequence 437, APP
7	46.5	36.9	1141	6	US-10-165-353A-437		Sequence 437, APP
8	46.5	36.9	1141	6	US-10-170-481A-437		Sequence 437, APP
9	46.5	36.9	1141	6	US-10-172-039A-437		Sequence 437, APP
10	46.5	36.9	1141	6	US-10-145-056A-437		Sequence 437, APP
11	46.5	36.9	1141	6	US-10-145-056A-437		Sequence 437, APP
12	46.5	36.9	1141	6	US-10-145-129A-437		Sequence 437, APP
13	46.5	36.9	1141	6	US-10-125-923A-120		Sequence 120, APP
14	46.5	36.9	1141	6	US-10-165-353A-437		Sequence 437, APP
15	46.5	36.9	1141	6	US-10-205-892-120		Sequence 120, APP
16	46.5	36.9	1141	6	US-10-174-575-120		Sequence 120, APP
17	46.5	36.9	1141	6	US-10-174-575A-120		Sequence 120, APP
18	46.5	36.9	1141	6	US-10-216-161A-437		Sequence 437, APP
19	46.5	36.9	1141	6	US-10-165-521A-437		Sequence 437, APP
20	46.5	36.9	1141	6	US-10-167-600-437		Sequence 437, APP
21	46.5	36.9	1141	6	US-10-187-755-120		Sequence 120, APP
22	46.5	36.9	1141	6	US-10-13-924-437		Sequence 437, APP
23	46.5	36.9	1141	6	US-10-013-928A-437		Sequence 437, APP
24	46.5	36.9	1141	6	US-10-167-600A-437		Sequence 437, APP
25	46.5	36.9	1141	6	US-10-187-749-120		Sequence 120, APP
26	46.5	36.9	1165	5	US-09-724-676A-75168		Sequence 75168, A

ALIGNMENTS

RESULT 1
US-10-092-411A-3614
; Sequence 3614, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032776-101
; CURRENT APPLICATION NUMBER: US-10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIORITY NUMBER: US 09/1134, 001
; PRIORITY FILING DATE: 1998-08-13
; PRIORITY APPLICATION NUMBER: US 60/064, 964
; PRIORITY FILING DATE: 1997-11-08
; PRIORITY FILING DATE: 1997-08-14
; SEQ ID NO: 3614
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-3614
; Sequence 437, Application US/10145087A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boststein, David
; APPLICANT: Destroyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Olang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PPIC7
 CURRENT APPLICATION NUMBER: US/10/145, 087A
 PRIORITY APPLICATION NUMBER: 09/918585
 PRIORITY FILING DATE: 2001-07-30
 PRIORITY APPLICATION NUMBER: 60/066364
 PRIORITY FILING DATE: 1997-10-17
 PRIORITY APPLICATION NUMBER: 60/064249
 PRIORITY FILING DATE: 1997-10-18
 PRIORITY APPLICATION NUMBER: 09/918585
 PRIORITY FILING DATE: 1997-11-13
 PRIORITY APPLICATION NUMBER: 60/066364
 PRIORITY FILING DATE: 1997-11-21
 PRIORITY APPLICATION NUMBER: 60/077450
 PRIORITY FILING DATE: 1997-11-03
 PRIORITY APPLICATION NUMBER: 60/077632
 PRIORITY FILING DATE: 1998-03-11
 PRIORITY APPLICATION NUMBER: 60/077641
 PRIORITY FILING DATE: 1998-03-11
 PRIORITY APPLICATION NUMBER: 60/077649
 PRIORITY FILING DATE: 1998-03-10
 PRIORITY APPLICATION NUMBER: 60/077791
 PRIORITY FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-10-145-087A-437

RESULT 3
 US-10-143-031A-437
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Oy 2 DLQERGDDNDI--SPFSGDQDPF 21
 || : | | | :|| ||:|
 Db 394 DLNQDGFPDIAGVAGPFDGDKVF 416

RESULT 4
 US-10-145-092A-437
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Oy 2 DLQERGDDNDI--SPFSGDQDPF 21
 || : | | | :|| ||:|
 Db 394 DLNQDGFPDIAGVAGPFDGDKVF 416

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-10-143-031A-437

GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kliavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paon, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630P1C45
 CURRENT APPLICATION NUMBER: US10/145,092A
 CURRENT FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-145-092A-437
 RESULT 5
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Qy 2 DQERGNDI--SPFSGDGQP 21
 Db 394 DLNQDGFPDIAVGAPFDGDKVF 416
 US-10-162-522A-437
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Qy 2 DQERGNDI--SPFSGDGQP 21
 Db 394 DLNQDGFPDIAVGAPFDGDKVF 416
 RESULT 6
 US-10-165-038A-437
 Sequence 437, Application US/10165038A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Olang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillen, Kenneth J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2630PIC29
 CURRENT APPLICATION NUMBER: US/10/165, 038A
 CURRENT FILING DATE: 2002-10-10
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 .PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO: 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-165-038A-437

RESULT 7
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Qy 2 DLQERGDNDI--SPPSGDGPF 21
 Db 394 DLNQDGFPDIAGVAGPFDGDKVF 416

US-10-165-353-437

Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Qy 2 DLQERGDNDI--SPPSGDGPF 21
 Db 394 DLNQDGFPDIAGVAGPFDGDKVF 416

RESULT 8
 US-10-170-481A-437
 Sequence 437, Application US/10/170481A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C53
 CURRENT APPLICATION NUMBER: US/10/170,481A
 CURRENT FILING DATE: 2002-10-10
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/0662250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO: 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-170-481A-437

Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

Qy 2 DQERGNDI--SPFSGDQPF 21
 ||| : ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
 Db 394 DLNQDGFPDIAVGAPFDGDKVF 416

RESULT 9
 US-10-172-039A-437

Sequence 437, Application US/10172039A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Boistein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C30
 CURRENT APPLICATION NUMBER: US/10/172,039A
 CURRENT FILING DATE: 2002-10-10
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/0662250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO: 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-172-039A-437

Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

Qy 2 DQERGNDI--SPFSGDQPF 21
 ||| : ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
 Db 394 DLNQDGFPDIAVGAPFDGDKVF 416

RESULT 10
 US-10-145-016A-437

Sequence 437, Application US/10145016A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Boistein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Sheldon, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P26301C52
 CURRENT APPLICATION NUMBER: US/10/145,016A
 CURRENT FILING DATE: 2001-10-18
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/07450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO 437
 LENGTH: 1141
 TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-145-016A-437

RESULT 11
 US 10-145-088A-437
 ; Sequence 437, Application US/10145088A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey E.
 ; APPLICANT: Godowski, Paul J.

Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 QY 2 DLQERGNDI--SPFSGDGQPF 21
 1| : ||| : ||| 111: ||| 111: |
 Db 394 DLNQDGFPDIAVGAPFDGKVF 416

US-10-145-088A-437
 ; ORGANISM: Homo sapiens
 ; US-10-145-088A-437

RESULT 12
 US 10-145-129A-437
 ; Sequence 437, Application US/10145129A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey E.
 ; APPLICANT: Godowski, Paul J.

Query Match 35.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 QY 2 DLQERGNDI--SPFSGDGQPF 21
 1| : ||| : ||| 111: ||| 111: |
 Db 394 DLNQDGFPDIAVGAPFDGKVF 416

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P3430R1C79
 CURRENT APPLICATION NUMBER: US/10/125,923A
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059266
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063120
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063121
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063486
 PRIOR FILING DATE: 1997-10-21
 PRIOR APPLICATION NUMBER: 60/063540
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063541
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063544
 PRIOR FILING DATE: 1997-10-28
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 120
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-145-929A-437
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 QY 2 DQBERGNDIT--SPFSGDQPF 21
 DB 394 DLNQDGFPDIAVGAPFDGDKVF 416
 RESULT 14
 US-10-165-353A-437
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 QY 2 DQBERGNDIT--SPFSGDQPF 21
 DB 394 DLNQDGFPDIAVGAPFDGDKVF 416
 RESULT 13
 US-10-125-923A-120
 Sequence 120, Application US/10125923A
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jia
 APPLICANT: Besnoyars, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: Acids Encoding the Same
 TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P263091C40
 CURRENT APPLICATION NUMBER: US710/165,353A
 PRIORITY FILING DATE: 2002-10-10
 PRIORITY APPLICATION NUMBER: 09/18585
 PRIORITY FILING DATE: 2001-07-30
 PRIORITY APPLICATION NUMBER: 60/062250
 PRIORITY FILING DATE: 1997-10-17
 PRIORITY APPLICATION NUMBER: 60/064249
 PRIORITY FILING DATE: 1997-11-03
 PRIORITY APPLICATION NUMBER: 60/065311
 PRIORITY FILING DATE: 1997-11-13
 PRIORITY APPLICATION NUMBER: 60/066364
 PRIORITY FILING DATE: 1997-11-21
 PRIORITY APPLICATION NUMBER: 60/07450
 PRIORITY FILING DATE: 1998-03-10
 PRIORITY APPLICATION NUMBER: 60/077632
 PRIORITY FILING DATE: 1998-03-11
 PRIORITY APPLICATION NUMBER: 60/077641
 PRIORITY FILING DATE: 1998-03-11
 PRIORITY APPLICATION NUMBER: 60/077649
 PRIORITY FILING DATE: 1998-03-11
 PRIORITY APPLICATION NUMBER: 60/077791
 PRIORITY FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO: 437
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-165-353A-437

RESULT 15
 US-10-205-892-120
 ; Sequence 120, Application US/10205892
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P243091C517
 CURRENT APPLICATION NUMBER: US/10/205,892
 CURRENT FILING DATE: 2002-07-26
 PRIORITY APPLICATION NUMBER: 10/053286
 PRIORITY FILING DATE: 2002-01-15
 PRIORITY APPLICATION NUMBER: 60/052263
 PRIORITY FILING DATE: 1997-09-18
 PRIORITY APPLICATION NUMBER: 60/052266
 PRIORITY FILING DATE: 1997-09-18
 PRIORITY APPLICATION NUMBER: 60/062250
 PRIORITY FILING DATE: 1997-10-17
 PRIORITY APPLICATION NUMBER: 60/063120
 PRIORITY FILING DATE: 1997-10-24
 PRIORITY APPLICATION NUMBER: 60/063121
 PRIORITY FILING DATE: 1997-10-24
 PRIORITY APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21
 PRIORITY APPLICATION NUMBER: 60/063540
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063541
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063544
 PRIORITY FILING DATE: 1997-10-28
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 120
 LENGTH: 1141
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-205-892-120
 Query Match 36.9%; Score 46.5; DB 6; Length 1141;
 Best Local Similarity 47.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Qy 2 DLQERGDNDT--SPFSGQOPF 21
 Db .394 DLNQDGFPDIAVGAPFDGDKVF 416

Search completed: January 17, 2003, 13:21:47
 Job time : 17 secs

Best Local Similarity 58.8%; Pred. No. 3.3%; Mismatches 5; Indels 0; Gaps 0; Query 1 TDLOERGDNNDISPRSGD 17
 ||| :||| :||| :|||
 Db 112 TDLDGGNDIPYLTGD 128

RESULT 3
 S36126 neural cell adhesion molecule L1 - rat
 N; Alternate names: nerve growth factor-inducible large external glycoprotein; NILE glycoprotein
 C; Species: *Rattus norvegicus* (Norway rat)
 C; Accession: S36126; S1655; A60917; A30326
 R; Miura, M.; Kobayashi, M.; Asou, H.; Uyemura, K.
 FEBs Lett. 289, 91-95, 1991
 A; Title: Molecular cloning of cDNA encoding the rat neural cell adhesion molecule L1. Two reference numbers: S17655; MUID:91372414; PMID:1894011
 A; Accession: S36126
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-1178 1183-1259 <MIU>
 A; Cross-references: EMBL:X59149; MUID:956740; PIDN:CAA41860.1; PID:956741
 R; Prince, J.T.; Milona, N.; Stallcup, W.B.
 J; Neurosci. 9, 1825-1834, 1989
 A; Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identification of a reference number: A60917; MUID:9257627; PMID:2723751
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1159-1199, 'G', 1201-1225, 'K', 1237 <PR1>
 A; Note: this paper appeared earlier, with printing errors, as reference A30326
 R; Prince, J.T.; Milona, N.; Stallcup, W.B.
 J; Neurosci. 9, 876-883, 1989
 A; Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identification of a reference number: A30326; MUID:9117485; PMID:2466966
 A; Contents: annotation
 C; Comment: This sequence of this surface-accessible glycoprotein differs at only two positions accessible only after treatment of cells with detergent and is assumed to be cytosolic
 C; Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; 1
 C; Keywords: cell adhesion; duplication; glycoprotein; membrane protein
 F; 531-592/Domain: immunoglobulin homology <NM>
 Query Match 39.3%; Score 49.5%; DB 2; Length 1259;
 Best Local Similarity 66.7%; Pred. No. 37%; Mismatches 1; Indels 4; Gaps 1;
 Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Query 2 DLQERGDNNDISPRSGDQ 19
 |||||||:||| :|||
 Db 558 DLQERGDNNDISPRSGDQ 574

RESULT 4
 AD322 Lyszyme (EC 3.2.1.17) - *Brucella melitensis* (strain 16M)
 C; Species: *Brucella melitensis*
 C; Accession: AD322 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
 R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Letete, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A; Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis* A; Reference number: AD3252; PMID:1756688
 A; Accession: AD322
 A; Status: preliminary
 A; Molecule type: DNA

RESULT 5
 D72858 late expression factor 3 - *Autographa californica* nuclear polyhedrosis virus
 C; Species: *Autographa californica* nuclear polyhedrosis virus, AcMNPV
 A; Note: dsDNA virus
 C; Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 24-Nov-1999
 C; Accession: D72858; A40577
 R; Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
 Virology 202, 586-605, 1994
 A; Title: The complete DNA sequence of *Autographa californica* nuclear polyhedrosis virus
 A; Reference number: A72850; MUID:94303173; PMID:803024
 A; Accession: D72858
 A; Molecule type: DNA
 A; Residues: 1-385 <IVR>
 A; Cross-references: GB:L22858; MUID:9510708; PIDN:AAA66697.1; PID:9559136
 R; Li, Y.; Passarelli, A.L.; Miller, L.K.
 J; Virol. 67, 5260-5268, 1993
 A; Title: Identification, sequence, and transcriptional mapping of lef-3, a baculovirus gene
 A; Reference number: A40677; MUID:93353600; PMID:3150397
 A; Accession: A40677
 A; Molecule type: DNA
 A; Residues: 1-385 <IVR>
 A; Cross-references: GB:L18873; MUID:9349019; PIDN:AAA02964.1; PID:9349020
 A; Note: authors translated the codon ACA for residue 92 as Tyr
 C; Genetics:
 A; Gene: Acc-lef3
 C; Keywords: transcription regulation
 Query Match 38.1%; Score 48%; DB 2; Length 385;
 Best Local Similarity 56.2%; Pred. No. 17%; Mismatches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Query 8 DNIDISPFSGDQPKD 23
 ||| :||| :||| :|||
 Db 61 DNK1OEVYQDSQSFKD 76

RESULT 6
 T41811 LEF-3 orf67 - *Bombyx mori* nuclear polyhedrosis virus (isolate T3)
 C; Species: *Bombyx mori* nuclear polyhedrosis virus, BmSNPV
 C; Accession: T41811
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 R; Gomi, S.; Majima, K.; Maeda, S.
 J; Gen. Virol. 80, 1323-1337, 1999
 A; Title: Sequence analysis of the genome of *Bombyx mori* nucleopolyhedrovirus.
 A; Reference number: 222020; MUID:99281911; PMID:1035780
 A; Accession: T41811
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-385 <RAM>
 A; Cross-references: EMBL:L33180; MUID:93745835; PIDN: AAC63740.1; PID:93745893
 A; Experimental source: isolate T3

C;Genetics: C;Note: ref-3

Query Match 38.1%; Score 48; DB 2; Length 385;
Best Local Similarity 56.2%; Pred. No. 17; Mismatches 9; Conservative 1; Indels 6; Gaps 0;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 DNDISPFSGQGPFKD 23
|| | : || | || |
Db 61 DNKIQBYYGQSQFKD 76

RESULT 7
B83891
intracellular alkaline serine proteinase aprx [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans*
C;Accession: B83891
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Title: Complete genome sequence of the alkaliophilic bacterium *Bacillus halodurans* and
R;Takami, H.; Nakagoe, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83891
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-444 <KUR>
A;Cross-references: GB:AA0001513; GB:BA000004; NID:910174345; PIDN:BA005649.1; GSPDB:GN00149
A;Experimental source: strain C-125
C;Genetics:
A;Gene: aprx

Query Match 37.3%; Score 47; DB 2; Length 444;
Best Local Similarity 47.1%; Pred. No. 28; Mismatches 8; Conservative 4; Indels 5; Gaps 0;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 DLQERGNDISPFSGQD 18
|| : | : | : | : |
Db 319 DTTDREDDVAPFESSRG 335

RESULT 8
AH0410
global stress requirement protein Gsra [imported] - *Yersinia pestis* (strain CO92)
C;Species: *Yersinia pestis*
C;Accession: AH0410
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002.
R;Parchall, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
depo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Snelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001.
A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0410
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-481 <KUR>
A;Cross-references: GB:AL590842; PIDN:CA092612.1; PID:915981308; GSPDB:GN00175
C;Genetics:
A;Gene: gsrA
C;Superfamily: Helicobacter serine proteinase

Query Match 37.3%; Score 47; DB 2; Length 481;
Best Local Similarity 62.5%; Pred. No. 30; Mismatches 10; Conservative 1; Indels 3; Gaps 1;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 7 GDNIDISPFSGQGPFK 22
|| | : || | || |
Db 80 GDN--SPFCQDGSPFQ 93

RESULT 9
B8944
hypothetical protein SA1447 [imported] - *Staphylococcus aureus* (strain N315)

Query Match 36.9%; Score 46.5%; DB 2; Length 1106;
Best Local Similarity 47.8%; Pred. No. 91; Mismatches 11; Conservative 3; Indels 6; Gaps 3;
Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 2 DLQERGNDI--SPFSGDQPF 21
|| : | : | : | : |
Db 362 DLNQDGFPDIAVGAPPFDGKVF 384

RESULT 10
S38783
Integrin alpha chain - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Accession: S38783; S23600
R;Kaufman, S.J.
submitted to the EMBL Data Library, March 1992
A;Reference number: S38783
A;Accession: S38783
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1106 <KAID>
A;Cross-references: EMBL:XA65036; NID:956392; PIDN:CAA46170.1; PID:956393
R;Song, W.K.; Wang, W.; Foster, R.F.; Bielser, D.A.; Kaufman, S.J.
J. Cell Biol. 117, 641-657, 1992.
A;Title: H36-alpha7 is a novel integrin alpha chain that is developmentally regulated
A;Reference number: S23600; MUID:92242309; PMID:1315319
A;Accession: S23600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 'R' 118-349, 'D', 351-804, 'R', 806, 'V', 808-1106 <SON>
A;Cross-references: EMBL:XA5036
C;Superfamily: Integrin alpha-2b chain

Query Match 36.9%; Score 46.5%; DB 2; Length 1106;
Best Local Similarity 47.8%; Pred. No. 91; Mismatches 11; Conservative 3; Indels 6; Gaps 3;
Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 2 DLQERGNDI--SPFSGDQPF 21
|| : | : | : | : |
Db 362 DLNQDGFPDIAVGAPPFDGKVF 384

RESULT 11
I61186
alpha-7 integrin - mouse
C;Species: *Mus musculus* (house mouse)
C;Accession: I61186
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Title: Alternative extracellular and cytoplasmic domains of the integrin alpha 7 subunit
A;Reference number: A49691; MUID:94075378; PMID:8253814
A;Accession: I61186
A;Status: preliminary; translated from GB/EMBL/MDBT

A;Molecule type: mRNA
 A;Residues: 1-1135 <RES>
 C;Superfamily: integrin alpha-2b chain

Query Match 36.9%; Score 46.5; DB 2; Length 1135;
 Best Local Similarity 47.8%; Pred. No. 94; Mismatches 6; Indels 3; Gaps 1;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 Qy 2 DLQRRGDNID--SPFSGDQPF 21
 || : || : || || : || || : || || : || ||
 Db 390 DLNQDGFPDIAVGAPFDGDKVF 412

RESULT 12

JC5550
 integrin alpha-7 chain precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 31-Dec-2000
 C;Accession: JC5550; J5951; A56319; S40147
 R;Lieung, E.; Lim, S.P.; Berg, R.; Yang, Y.; Ni, J.; Wang, S.; Krissansen, G.W.
 Biochem. Biophys. Res. Commun. 243, 317-325, 1998
 A;Title: A novel extracellular domain variant of the human integrin alpha 7 subunit gene
 A;Reference number: JC5550; MUID:98139911; PMID:9473524
 A;Accession: JC5550
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: GB:AF032108
 A;Cross-references: GB:AF032108; NID:92897115; PIDN:AKC39708.1; PID:92897116
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1137 <LEU1>
 A;Cross-references: GB:AF032108
 A;Cross-references: GB:AF032108; NID:92897115; PIDN:AKC39708.1; PID:92897116
 A;Reference number: A56839
 A;Accession: A56839
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 664-666, 668-688, 690-825, 'X', 827-839, 'D', 841-946, 'H', 948, 'T', 951, 'P', 953-1052
 A;Cross-references: EMBL:XA4295; NID:9437781
 R;Song, W.K.; Wang, W.; Sato, H.; Bieleser, D.; Kaufman, S.
 submitted to the EMBL Data Library, July 1993
 A;Description: Expression of alpha 7 integrin cytoplasmic domains during skeletal muscle
 hophotoses.
 A;Reference number: S40147
 A;Accession: S40147
 A;Molecule type: mRNA
 A;Residues: 1061-1137 <SON>
 A;Cross-references: EMBL:XY4295; NID:9437781; PIDN:CAA52348.1; PID:9437782
 C;Genetics:

A;Gene: GDB:ITGA7
 A;Cross-references: GDB:131465; OMIM:600536
 A;Map position: 12q13-12q13
 C;Superfamily: integrin alpha-2b chain
 C;Keywords: glycoprotein; skeletal muscle; transmembrane protein
 F;1-33/Domain: signal sequence #status predicted <SG>
 F;34-1137/Product: integrin alpha-7 chain, long splice form #status predicted <M41L>
 F;1038-1056/Domain: integrin alpha-7 chain, short splice form #status predicted <TRM>
 F;86-742,945,981,1001/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 36.9%; Score 46.5; DB 2; Length 1137;
 Best Local Similarity 47.8%; Pred. No. 94; Mismatches 6; Indels 3; Gaps 1;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

Qy 2 DLQRRGDNID--SPFSGDQPF 21
 || : || : || || : || || : || || : || ||
 Db 390 DLNQDGFPDIAVGAPFDGDKVF 412

RESULT 13

AD3154
 nucleotidyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C;Accession: AD3154
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McCle
 Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:11743193
 A;Accession: AB3154
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AE008689; PIDN:AKL45650.1; PID:917743374; GSDDB:GN00187
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu4856
 A;Map position: linear chromosome

Query Match 36.5%; Score 46; DB 2; Length 308;
 Best Local Similarity 60.0%; Pred. No. 26; Mismatches 5; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 7 GDNDISPFSGDQPF 21
 || : || : || || : || || : || ||
 Db 112 GARRISNLNDGQPF 126

RESULT 14

E98133
 hypothetical protein AGR_L_62 [imported] - Agrobacterium tumefaciens (strain C58, cer
 C;Species: Agrobacterium tumefaciens
 C;Accession: E98133
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldm
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
 A;Reference number: E98133
 A;Accession: E98133
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-365 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AK88591.1; PID:915158304; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L_62
 A;Map position: linear chromosome

Query Match 36.5%; Score 46; DB 2; Length 365;
 Best Local Similarity 60.0%; Pred. No. 32; Mismatches 5; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 7 GNDISPFSGDQPF 21
 || : || : || || : || || : || ||
 Db 169 GAREISNLNDQPF 183

RESULT 15

AB3170
 Sadenosylmethionine-tRNA ribosyltransferase-1somerase (EC 5.4.99.-) queA PA3824 [sim
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: AB3170
 R;Stover, C.C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa

A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: A83170
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-347 <STO>
A; Cross-references: GB:AE004799; GB:AE004091; NID:99949981; PIDN:AA07211.1; GSPDB:GN001
A; Experimental source: strain PA01
C; Genetics:
A; Gene: queA; PA3024
C; Superfamily: Escherichia coli tRNA ribosyltransferase-isomerase
C; Keywords: intramolecular transferase; isomerase

Query Match 36.1%; Score 45.5; DB 2; Length 347;
Best Local Similarity 42.9%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;
Qy 8 DNNDISPPSGD----GQPF 21
| :: ||||| |:|
Db 263 DGEALKPPSGDTIYPGRPF 283

Search completed: January 17, 2003, 13:17:03
Job time : 18 secs

Copyright (c) 1993 - 2003 Compugen Ltd.										GenCore version 5.1.3			
OM protein - protein search, using sw model										MIPD_ECOLI			
Run on: January 17, 2003, 13:16:38 ; Search time 10 Seconds										HRCA_RHIME			
(without alignments)										P02511_drosophila			
Title: US-09-641-034-47										P04239_rhizobium_m			
Perfect score: 126										P09850_deinococcus			
Sequence: 1 TDQEQGDNDISPFSQDGQPRKD 23										P03250_mycobacteri			
Scoring table: BLOSUM62										P14565_escherichia			
Gapop 10.0 , Gapext 0.5										P20313_bacterioph			
Database : SwissProt; 40.4*										P33702_escherichia			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										P060116_schizosacch			
SUMMARIES										P49714_bacterioph			
Result No. Score Query Match Length DB ID Description										P53708_homo_sapien			
RESULT 1													
PORI_RHOCA		STANDARD;		PRT;		301 AA.		RN					
ID PORT_RHOCA		P31243;		DT		01-JUL-1993 (Rel. 26, Created)		RN					
AC P03695		DT		01-JUL-1993 (Rel. 26, Last sequence update)		RN		RN					
Minimum DB seq length: 0		DT		01-OCT-1994 (Rel. 30, Last annotation update)		DE		RN					
Maximum DB seq length: 2000000000		DE		Porin.		OS		RN					
Post-processing: Minimum Match 0%		OS		Rhodobacter capsulatus (Rhodopseudomonas capsulata).		OC		RN					
Maximum Match 100%		OC		Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;		OC		RN					
Listing first 45 summaries		OC		Rhodobacter.		OX		RN					
NCBI-TaxID=1061;		OX		[1]		RN		RN					
SEQUENCE.		RN		RN		RN		RN					
STRAIN=DSM 938 / 37b4;		RX		MEDLINE=91330909; PubMed=1651239;		RN		RN					
"Primary structure of porin from Rhodobacter capsulatus.";		RN		Schiltz E., Kreusch A., Nestel U., Schulz G.E.;		RN		RN					
[2]		RN		"The three-dimensional structure of porin from Rhodobacter capsulatus at 3-A resolution.";		RN		RN					
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).		RN		P11622; Lett. 267:268-272(1990).		RN		RN					
X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).		RN		X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).		RN		RN					
STRAIN=DSM 938 / 37b4;		RX		MEDLINE=9112174; PubMed=1707373;		RN		RN					
"The structure of porin from Rhodobacter capsulatus at 1.8-A resolution.";		RN		Weiss M.S., Wacker T., Weckesser J., Walte W., Schulz G.E.;		RN		RN					
"The structure of porin from Rhodobacter capsulatus at 1.8-A resolution.";		RN		Weiss M.S., Kreusch A., Schulz G.E., Nestel U., Walte W., Weckesser J., Schulz G.E.;		RN		RN					
[3]		RN		"The structure of porin from Rhodobacter capsulatus at 1.8-A resolution.";		RN		RN					
FEBs Lett. 280:379-382(1991).		RN		X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).		RN		RN					
[4]		RN		MEDLINE=93021091; PubMed=11328651;		RN		RN					
"Structure of porin refined at 1.8-A resolution.";		RN		Weiss M.S., Schulz G.E.;		RN		RN					
Structure of porin refined at 1.8-A resolution.";		RN		"Structure of porin refined at 1.8-A resolution.";		RN		RN					
J. Mol. Biol. 227:493-509(1992).		RN		J. Mol. Biol. 227:493-509(1992).		RN		RN					
FUNCTION: FORMS CHANNELS THAT ALLOW THE PASSIVE DIFFUSION OF SMALL		CC		FUNCTION: FORMS CHANNELS THAT ALLOW THE PASSIVE DIFFUSION OF SMALL		CC		RN					
HYDROPHILIC SOLUTES UP TO AN EXCLUSION LIMIT OF ABOUT 0.6 KDA.		CC		HYDROPHILIC SOLUTES UP TO AN EXCLUSION LIMIT OF ABOUT 0.6 KDA.		CC		RN					
SUBUNIT: HOMOTIMER.		CC		SUBUNIT: HOMOTIMER.		CC		RN					
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.		CC		SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.		CC		RN					
- DOMAIN: THE MONOMER CONSISTS OF A 16-STRANDED ANTI-PARALLEL BETA-		CC		- DOMAIN: THE MONOMER CONSISTS OF A 16-STRANDED ANTI-PARALLEL BETA-		CC		RN					
PLEATED SHEET BARREL (171 RESIDUES), THREE SHORT ALPHA-HELICES (18		CC		PLEATED SHEET BARREL (171 RESIDUES), THREE SHORT ALPHA-HELICES (18		CC		RN					
RESIDUES) AND 13 HYDROGEN-BONDED REVERSE TURNS (26 RESIDUES).		CC		RESIDUES) AND 13 HYDROGEN-BONDED REVERSE TURNS (26 RESIDUES).		CC		RN					
PDB: 1S10; 2P0R; 3P10.		PDB: 1S10; 2P0R; 3P10.		PDB: 1S10; 2P0R; 3P10.		PDB: 1S10; 2P0R; 3P10.		RN					
PDB: 3POR; 15-JUL-93.		PDB: 3POR; 15-JUL-93.		PDB: 3POR; 15-JUL-93.		PDB: 3POR; 15-JUL-93.		RN					
Outer membrane; Transmembrane; Porin; 3D-structure.		STRAND		Outer membrane; Transmembrane; Porin; 3D-structure.		STRAND		RN					
FT		FT		FT		FT		RN					
TURN		TURN		TURN		TURN		RN					
36		37		37		37		RN					

FT	STRAND	40	46	CC
FT	HELIX	47	53	CC
FT	TURN	54	56	CC
FT	STRAND	55	60	CC
FT	TURN	60	65	CC
FT	STRAND	66	67	CC
FT	STRAND	68	73	CC
FT	HELIX	78	83	CC
FT	TURN	90	93	CC
FT	TURN	96	97	CC
FT	TURN	97	108	CC
FT	TURN	111	112	CC
FT	HELIX	113	115	CC
FT	STRAND	115	125	CC
FT	TURN	118	127	CC
FT	STRAND	126	128	CC
FT	TURN	134	139	CC
FT	TURN	140	141	CC
FT	STRAND	142	142	CC
FT	STRAND	148	158	CC
FT	TURN	159	160	CC
FT	STRAND	161	168	CC
FT	STRAND	171	173	CC
FT	TURN	177	179	CC
FT	STRAND	183	194	CC
FT	TURN	195	196	CC
FT	STRAND	197	209	CC
FT	HELIX	210	216	CC
FT	TURN	217	218	CC
FT	STRAND	228	242	CC
FT	TURN	243	244	CC
FT	STRAND	245	256	CC
FT	TURN	257	259	CC
FT	STRAND	260	274	CC
FT	TURN	275	276	CC
FT	STRAND	277	286	CC
FT	STRAND	294	301	CC
SQ	SEQUENCE	301 AA:	31536 MW:	4C57149C348D2943 CRC64:
Query	Match	41.3%;	Score 52;	DB 1;
Best	Local Similarity	58.8%;	Pred. No. 0.99;	Length 301;
Matches	10;	Conservative	2;	Mismatches 5;
QY	1	TDLQERQEDNDNIDSPFSGD	17	Indels 0;
Db	92	TDLDDDRGGNDIDPYLTD	108	Gaps 0;
RESULT	2			
CAML	RAT	STANDARD;	PRT;	1259 AA.
AC	005695;	01-FEB-1994 (Rel. 28, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neural cell adhesion molecule LI Precursor (NCAM LI).			
GN	CAMLI			
OS	Rattus norvegicus (Rat).			
OC	Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
	MEDLINE-91372414; PubMed-1894011; Miura M., Kobayashi M., Asou H., Uyemura K.; "Molecular cloning of cDNA encoding the rat neural cell adhesion molecule LI. Two LI isoforms in the cytoplasmic region are produced by differential splicing"; FEBS Lett. 289:91-95(1991). -1- FUNCTION: CELL ADHESION MOLECULE WITH AN IMPORTANT ROLE IN THE DEVELOPMENT OF THE NERVOUS SYSTEM, INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS TO AXONIN ON NEURONS. -1- SUBCELLULAR LOCATION: Type I membrane protein.			

FT CARBOHYD 1106 1106 N-LINKED (GLCNAC-¹)- (POTENTIAL).
 FT VARSPLIC 1179 1182 MISSING (IN ISFORM 2).
 SQ SEQUENCE 1259 AA; 140934 MW; OF12AVC4415F3C0B CRC64;
 Best Local Similarity 39.3%; Score 49.5; DB 1; Length 1259;
 Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 QY |||||||:||||||| 19
 Db 558 DLQERGDNDLSPFFSGDQ 19
 |||||||:||||||| 574

RESULT 3

LEF3_NPVAC STANDARD; PRT; 385 AA.
 ID LEF3_NPVAC
 AC P4153;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Late expression factor 3.
 GN LEF-3.
 OS Autographa californica nuclear polyhedrosis virus (ACMNPV).
 OX Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=46015;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=L1;
 RX MEDLINE=93353600; PubMed=8350397;
 RA Li Y., Passarelli A.L., Miller L.K.;
 RT "Identification, sequence, and transcriptional mapping of lef-3, a
 baculovirus gene involved in late and very late gene expression.";
 RL J. Virol. 67:2260-2268(1993).
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=CC;
 RX MEDLINE=94303173; PubMed=8030224;
 RA Ayles M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear
 polyhedrosis virus";
 RL Virology 202:586-605(1994).
 -1- FUNCTION: REQUIRED FOR LATE AND VERY LATE GENE EXPRESSION. LEF-3
 COULD BE A SINGLE STRANDED DNA-BINDING PROTEIN.

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; L1887; AAA02964.1; -
 DR EMBL; L22858; AAA66697.1; -
 DR PIR; A40677; A40677;
 KW Early protein; Transcription regulation; DNA-binding;
 SEQUENCE 385 AA; 4451 MW; 9A15ECDDBA7F0DF1 CRC64;

Query Match 38.1%; Score 48; DB 1; Length 385;
 Best Local Similarity 56.2%; Pred. No. 5.5;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY |||||:||||||| 23
 Db 61 DNKQEYQGDSQSFKD 76

RESULT 4

ITAT_RAT STANDARD; PRT; 1106 AA.
 ID ITAT_RAT
 AC 063258; Q63026; Q65027;
 DT 16-OCT-2001 (Rel. 40, Created)

FT 16-OCT-2001 (Rel. 40, Last sequence update)
 FT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interulin alpha-7 (H36-alpha7).
 GN ITGA1.
 OS Rattus norvegicus (Rat).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-7X1B).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=92242309; PubMed=1315319;
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=9417194; PubMed=8126096;
 RA Song W.K., Wang W., Foster R.F., Bielser D.A., Kaufman S.J.;
 RA Song W.K., Wang W., Sato H., Bielser D.A., Kaufman S.J.;
 RT "Expression of alpha-7 integrin cytoplasmic domains during skeletal
 muscle development: alternate forms, conformational change, and
 RT homologies with serine/threonine kinases and tyrosine phosphatases.";
 RL J. Cell Sci. 106:1139-1152(1993).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=9619713; PubMed=8626012;
 RA Martin P.T., Kaufman S.J., Kramer R.H., Sanes J.R.;
 RT "Synaptic interlins in developing, adult, and mutant muscle: selective
 association of alpha1, alpha7A, and alpha7B integrins with the
 neuromuscular junction.";
 RL Dev. Biol. 174:125-139(1996).
 CC CC
 CC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC
 DIFFERENTIATION, IT MAY INDUCE CHANGES IN THE SHAPE AND MOBILITY
 OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH
 SITES OF SECONDARY FIBER FORMATION. INVOLVED IN THE MAINTENANCE OF
 THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR ANCHORAGE.
 CC CC
 CC -1- SUBUNIT: HETEROODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
 SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
 DISULFIDE BOND. ALPHA-7 ASSOCIATES WITH BETA-1.
 CC CC
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC CC
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; ALPHA-7X1A, ALPHA-7X1B
 (SHOWN HERE) AND ALPHA-7X1C; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC CC
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL AND CARDIAC MUSCLE.
 CC EXPRESSED IN REPLICATING MYOBLASTS. IN DIFFERENTIATED MUSCLE
 CC FIBERS LOCALIZES BETWEEN FIBERS AND THE SURROUNDING MATRIX.
 CC ISOFORMS A AND B ARE EXPRESSED AT MYOTENDONOUS AND NEUROMUSCULAR
 CC JUNCTIONS; ISOFORM C IS EXPRESSED AT NEUROMUSCULAR JUNCTIONS AND
 CC AT EXTRASYNAPTIC SITES.
 CC CC
 CC -1- DEVELOPMENTAL STAGE: ISOFORMS ARE DEVELOPMENTALLY REGULATED DURING
 CC THE FORMATION OF SKELETAL MUSCLE. ISOFORMS A AND C ARE INDUCED
 CC UPON TERMINAL MYOGENIC DIFFERENTIATION; ISOFORM B IS PRESENT
 CC EARLIER IN REPLICATING CELLS AND DIMINISHES UPON DIFFERENTIATION.
 CC -1- PTM: ADP-RIBOSYLATED ON AT LEAST TWO SITES IN THE EXTRACELLULAR
 CC DOMAIN IN SKELETAL MYOFIBERS (BY SIMILARITY).
 CC CC
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA-CHAIN FAMILY.
 CC CC
 CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC CC
 CC EMBL; X65036; CAA46170.1; -
 DR EMBL; X74293; CAA5246.1; -
 DR EMBL; X74294; CAA5247.1; -
 DR HSSP; P11215; 1A8X.

DR	Interpro; IPR000413; Integrin-alpha.
PFAM	PF00357; integrin_A; 1.
DR	Pfam; PF01839; FG-GAP; 5.
PRINTS	PRO1BS; INTEGRINA.
SMART	SM00191; Int_alpha; 5.
PROSITE	PS0042; INTEGRIN_ALPHA; 1.
KW	Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Receptor; Alternative splicing; ADP-ribosylation; Calcium.
CHAIN	1 882 INTEGRIN ALPHA-7 HEAVY CHAIN (POTENTIAL).
DOMAIN	1 1003 EXTRACELLULAR (POTENTIAL).
TRANSMEM	1004 1029 CYTOPLASMIC (POTENTIAL).
DOMAIN	1030 1106 CYTOPLASMIC (POTENTIAL).
REPEAT	17 55 FG-GAP 1.
REPEAT	90 122 FG-GAP 2.
REPEAT	162 194 FG-GAP 3.
REPEAT	233 269 FG-GAP 4.
REPEAT	290 328 FG-GAP 5.
REPEAT	351 387 FG-GAP 6.
REPEAT	409 449 FG-GAP 7.
CA_BIND	300 308 POTENTIAL.
CA_BIND	362 370 POTENTIAL.
CA_BIND	420 428 POTENTIAL.
DOMAIN	880 885 POLY-ARG.
SITE	1032 1036 GFFKR MOTIF.
DOMAIN	1082 1101 3 X 4 AA REPEATS OF D-X-H-P.
REPEAT	1082 1085 1.
REPEAT	1090 1093 2.
REPEAT	1098 1101 3.
DISULFID	61 71 BY SIMILARITY.
DISULFID	108 131 BY SIMILARITY.
DISULFID	152 165 BY SIMILARITY.
DISULFID	467 474 BY SIMILARITY.
DISULFID	543 543 BY SIMILARITY.
DISULFID	609 615 BY SIMILARITY.
DISULFID	719 720 BY SIMILARITY.
DISULFID	866 920 INTERCHAIN (BY SIMILARITY).
DISULFID	926 931 BY SIMILARITY.
CARBONYD	713 713 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBONYD	915 915 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBONYD	950 950 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBONYD	970 970 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARSPPLIC	1031 1106 LGFPEKRAKPEAKPTVYHAWKILRERDQKEEKIGIORS
FT	NWGNQWEGSDAHTLAAQWHPGPQDGHVSVA -> CG
FT	FRRNQSPSSPSSPANHRAVQDQPSAAMEAGGGTQWGDSS
FT	GRSFLRPLKPSTO (IN ISOFORM ALPHA-7(X1A)).
FT	RAKHFEPATVQYHAWKILRERDQKEEKIGIORSNWGS
FT	QWEQSDAHTLAAQWHPGPQDGHVSVA -> CAVPAQR
FT	ILSTY (IN ISOFORM ALPHA-7(X1C)).
SO	SEQUENCE 1106 AA; 121101 MW; 21B2A187837E01F6 CRC64;
Query Match	36.9%; Score 46.5; DB 1; Length 1106;
Best Local Similarity	47.8%; Pred. No. 32;
Matches	11; Conservative
Qy	2 DIQERGNDI---SPFSGDQGP 21
Db	362 DLNQDGFDPDIAVGAPFQDGKVF 384
RESULT 5	
ITR7_MOUSE	STANDARD; PRT; 1179 AA.
ID	ITR7_MOUSE
AC	061738; P70350; 088732; Q61737; 088731; Q61741;
DT	16-OCT-2001 (Rel. 40, created)
DT	16-OCT-2001 (Rel. 40, last sequence update)
DT	15-JUN-2002 (Rel. 41, last annotation update)
DE	Integrin alpha-7 precursor.
GN	ITGA7.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	NCBIL TAXID=10090;
OX	
ITR7_MOUSE	SEQUENCE FROM N.A. (ISOFORMS ALPHA-7A; ALPHA-7X2B AND ALPHA-7X1X2).
ITR7_MOUSE	SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X1X2A AND ALPHA-7X1X2B).
ITR7_MOUSE	"Alternative extracellular and cytoplasmic domains of the integrin alpha 7 subunit are differentially expressed during development.";
ITR7_MOUSE	J. Biol. Chem. 268: 26773-26783 (1993).
ITR7_MOUSE	[12]
ITR7_MOUSE	SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X1X2A AND ALPHA-7X1X2B).
ITR7_MOUSE	SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X1X2A AND ALPHA-7X1X2B).
ITR7_MOUSE	"Genomic organization and chromosomal localization of the mouse integrin alpha7 gene.";
ITR7_MOUSE	Submitted. (APR-1997) to the EMBL/GenBank/DBJ databases.
ITR7_MOUSE	[13]
ITR7_MOUSE	SEQUENCE OF 1-70 FROM N.A.
ITR7_MOUSE	[4]
ITR7_MOUSE	STRAIN=C57BL/6 X CBA;
ITR7_MOUSE	MEDLINE=96394366; PubMed=8798472;
ITR7_MOUSE	Zilberman B.L., Kramer R.H.;
ITR7_MOUSE	"Identification and characterization of the cell type-specific and developmentally regulated alpha7 integrin gene promoter.";
ITR7_MOUSE	J. Biol. Chem. 271: 22915-22922 (1996).
ITR7_MOUSE	[4]
ITR7_MOUSE	SEQUENCE OF 34-58.
ITR7_MOUSE	SEQUENCE OF 34-58.
ITR7_MOUSE	TISSUE=Melanoma;
ITR7_MOUSE	MEDLINE=92198982; PubMed=1839357;
ITR7_MOUSE	Kramer R.H., Vu M.P., Cheng Y.F., Ramos D.M., Timpl R., Walch N.;
ITR7_MOUSE	"Laminin-binding integrin alpha 7 beta 1: functional characterization and expression in normal and malignant melanocytes.";
ITR7_MOUSE	Cell Regul. 2: 805-817 (1991).
ITR7_MOUSE	[15]
ITR7_MOUSE	DISULFID
ITR7_MOUSE	PARTIAL SEQUENCE FROM N.A. (ISOFORMS ALPHA-7A AND ALPHA-7B).
ITR7_MOUSE	STRAIN=C57BL/6 X BALB/C;
ITR7_MOUSE	RX
ITR7_MOUSE	COLL G., Starr L., Quaranta V.;
ITR7_MOUSE	"A new isoform of the laminin receptor integrin alpha 7 beta 1 is developmentally regulated in skeletal muscle.";
ITR7_MOUSE	J. Biol. Chem. 268: 19019-19024 (1993).
ITR7_MOUSE	[16]
ITR7_MOUSE	TISSUE SPECIFICITY.
ITR7_MOUSE	MEDLINE=96197133; PubMed=8360188;
ITR7_MOUSE	Martin P.T., Kaufman S.J., Kramer R.H., Sano J.R.;
ITR7_MOUSE	"Synaptic integrins in developing, adult, and mutant muscle: selective association of alpha1, alpha7, and alpha7B integrins with the neuromuscular junction.";
ITR7_MOUSE	Dev. Biol. 174: 125-139 (1996).
ITR7_MOUSE	[17]
ITR7_MOUSE	FUNCTION.
ITR7_MOUSE	MEDLINE=98016417; PubMed=9354797;
ITR7_MOUSE	Mayer U., Sauer G., Fassler R., Bornemann A., Echtermeyer F.,
ITR7_MOUSE	"Absence of integrin alpha 7 causes a novel form of muscular dystrophy.";
ITR7_MOUSE	Nat. Genet. 17: 318-323 (1997).
ITR7_MOUSE	[18]
ITR7_MOUSE	ADP-RIBOSYLATION.
ITR7_MOUSE	MEDLINE=95238432; PubMed=7721841;
ITR7_MOUSE	Zolotowska A., Moss J.;
ITR7_MOUSE	"Processing of ADP-ribosylated Integrin alpha 7 in skeletal muscle myotubes.";
ITR7_MOUSE	RL J. Biol. Chem. 270: 9227-9233 (1995).
ITR7_MOUSE	-1- FUNCTION: INTEGRIN ALPHA-7/BETA-1 IS THE PRIMARY LAMININ RECEPTOR ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC DIFFERENTIATION, IT MAY INDUCE CHANGES IN THE SHAPE AND MOBILITY OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH SITES OF SECONDARY FIBER FORMATION. INVOLVED IN THE MAINTENANCE OF THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR ANCHORAGE, VIABILITY AND FUNCTIONAL INTEGRITY. MICE CARRYING A ITGA7 NULL ALLELE ARE Viable AND FERTILE, BUT SHOW PROGRESSIVE MUSCULAR DYSTROPHY STARTING SOON AFTER BIRTH, BUT WITH A DISTINCT VARIABILITY IN DIFFERENT MUSCLE TYPES.

RT subunit generated by alternative intron splicing.";

RL *Biochem. Biophys. Res. Commun.* 243:317-325(1998).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2B).

RX MEDLINE-98250181; published-950229;

RA Hayashi Y.K., Chou F.-L., Engvall E., Ogawa M., Matsuda C., RA Kramer R.H., Kaufman S.J., Hoffmann E.P., Arshava K., RA Ozawa E., Goto Y.-I., Nonaka I., Tsukahara T., Wang J.Z., RA Nat. Genet. 19:94-97(1998).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2B).

RA Vizirianakis I.S., Ziobor B.L., Kramer R.H., RT "Mutations in the integrin alpha7 gene cause congenital myopathy.";

RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE-Skeletal muscle;

RX MEDLINE-99335684; published-10403775;

RA Vignier N., Moghadzadeh B., Gary F., Beckmann J., Mayer U., RT "Cloning of human integrin alpha7 cDNA.";

RL "Structure, genetic localization, and identification of the cardiac and skeletal muscle transcripts of the human integrin alpha7 gene (ITGA7)." ;

RC *Biochem. Biophys. Res. Commun.* 260:357-364(1999).

RN [5]

RP SEQUENCE OF 34-45.

RC TISSUE-Melanoma;

RX MEDLINE-92198982; published-10339357;

RA Kramer R.H., Vu M.P., Cheng Y.F., Ramos D.M., Timpl R., Walsh N., RT "Laminin-binding integrin alpha7/beta1: functional characterization and expression in normal and malignant melanocytes.";

RL Cell Regul. 2:805-817(1991).

RN [6]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2).

RC TISSUE-Heart;

RX MEDLINE-94075378; published-8253814;

RA Ziobor B.L., Vu M.P., Waleh N., Crawford J., Lin C.-S., Kramer R.H., RT "Alternative extracellular and cytoplasmic domains of the integrin alpha7 subunit are differentially expressed during development.";

RT *J. Biol. Chem.* 268:26773-26783(1993).

RN [7]

RP SEQUENCE OF 1105-1181 FROM N.A. (ISOFORM ALPHA-7B).

RC TISSUE-Fetal muscle;

RX MEDLINE-94111924; published-8126096;

RA Song W.K., Wang W., Sato H., Bleiser D.A., Kaufman S.J., RT "Expression of alpha7 integrin cytoplasmic domains during skeletal muscle development: alternate forms, conformational change, and homologies with serine/threonine kinases and tyrosine phosphatases.";

RT *J. Cell Sci.* 106:1139-1152(1993).

RN [8]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-7A).

RC TISSUE-Skeletal muscle;

RX MEDLINE-98012902; published-9352853;

RA Basora N., Vachon P.H., Herring Gillam F.E., Perreault N., RA Beaulieu J.-F., RT "Relation between integrin alpha7beta1 expression in human intestinal cells and enterocytic differentiation." ;

RT *Gastroenterology* 113:1510-1521(1997).

RN [9]

RP FUNCTION

RX MEDLINE-97453229; published-9307969;

RA Ziobor B.L., Chen Y.Q., Kramer R.H., RT "The laminin-binding activity of the alpha7 integrin receptor is defined by developmentally regulated splicing in the extracellular domain.";

RT *Mol. Biol. Cell* 8:1723-1734(1997).

RN [10]

RP FUNCTION

RX MEDLINE-20160722; published-1069445;

RA Schober S., Mielenz D., Echtermeyer F., Hapke S., Poeschl E., von der Mark H., Moch H., von der Mark K.,

RT "The role of extracellular and cytoplasmic splice domains of alpha7-integrin in cell adhesion and migration on laminins.";

RL *Exp. Cell Res.* 255:303-313(2000).

RN [11]

RP TISSUE-SPECIFICITY.

RX MEDLINE-96197133; PubMed-8626012;

RA Martin P.T., Kaufman S.J., Kramer R.H., Sanes J.R., RT "Synaptic integrins in developing, adult, and mutant muscle: selective association of alpha1, alpha7A, and alpha7B integrins with the neuromuscular junction";

RL *Dev. Biol.* 174:1125-1139(1996).

CC CC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC DIFFERENTIATION, IT MAY INDUCE CHANGES IN THE SHAPE AND MOBILITY OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH SITES OF SECONDARY FIBER FORMATION. IT IS INVOLVED IN THE MAINTENANCE OF THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR ANCHORAGE, VIABILITY AND FUNCTIONAL INTEGRITY. ISOFORMS ALPHA-7X2B AND ALPHA-7X1B PROMOTE MYOBLAST MIGRATION ON LAMININ 1 AND LAMININ 2/4, BUT ALPHA-7X1B IS LESS ACTIVE ON LAMININ 1 (IN VITRO).

CC CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULFIDE BOND. ALPHA-7 ASSOCIATES WITH BETA-1.

CC CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.

CC CC -1- ALTERNATIVE PRODUCTS: TYPE I membrane protein; ALPHA-7X1B, ALPHA-7X1DA, ALPHA-7X1DB, ALPHA-7X2A, ALPHA-7X2B, ALPHA-7X2DA, ALPHA-7X2DB, ALPHA-7X1X2A, ALPHA-7X1X2B (SHOWN HERE), ALPHA-7X1X2A AND ALPHA-7X1X2B; MAY BE PRODUCED BY ALTERNATIVE SPlicing. THERE IS A COMBINATION OF AT LEAST FIVE ALTERNATIVE CYTOPLASMIC DOMAINS, THREE EXTRACELLULAR (X1, X2 AND D) AND TWO CYTOPLASMIC (A AND B). A THIRD POTENTIAL ALTERNATIVE SPliced CYTOPLASMIC DOMAIN (C) DOES NOT APPEAR TO BE EXPRESSED. IN VITRO GENERATED ISOFORM X2C SHOWS FUNCTION. SO FAR DETECTED ARE ISOFORMS ALPHA-7X1A, ALPHA-7X1B (MAJOR), ALPHA-7X2B (MINOR) AND MINOR ISOFORMS CONTAINING SEGMENT X1X2.

CC CC -1- TISSUE-SPECIFICITY: ISOFORMS CONTAINING SEGMENT A ARE PREDOMINANTLY EXPRESSED IN SKELETAL MUSCLE. ISOFORMS CONTAINING SEGMENT B ARE ABUNDANTLY EXPRESSED IN SKELETAL MUSCLE, MODERATELY IN CARDIAC MUSCLE, SMALL INTESTINE, COLON, OVARY AND PROSTATE AND WEAKLY IN LUNG AND TESTES. ISOFORMS CONTAINING SEGMENT X2D ARE EXPRESSED AT LOW LEVELS IN FETAL AND ADULT SKELETAL MUSCLE AND IN CARDIAC MUSCLE, BUT ARE NOT DETECTED IN MYOBLASTS AND MYOTYPES. IN MUSCLE FIBERS ISOFORMS CONTAINING SEGMENT A AND B ARE EXPRESSED AT MYOENDODIUS AND NEUROMUSCULAR JUNCTIONS; ISOFORMS CONTAINING SEGMENT C ARE EXPRESSED AT NEUROMUSCULAR JUNCTIONS AND AT EXTRASINAPTIC SITES. ISOFORMS CONTAINING SEGMENTS X1 OR X2 OR, AT LOW LEVELS, X1X2 ARE EXPRESSED IN FETAL AND ADULT SKELETAL MUSCLE (MYOBLASTS AND MYOTYPES) AND CARDIAC MUSCLE.

CC CC -1- DEVELOPMENTAL STAGE: IN RENEWING INTESTINAL EPITHELIUM, EXPRESSION OF ISOFORMS CONTAINING SEGMENT B CORRELATES WITH THE ONSET OF ENTEROCYTIC DIFFERENTIATION.

CC CC -1- PTM: ADD RIBOSYLATED ON AT LEAST TWO SITES OF THE EXTRACELLULAR DOMAIN IN SKELETAL MYOTYPES (BY SIMILARITY).

CC CC -1- DISEASE: DEFECTS IN ITGA7 ARE ASSOCIATED WITH A FORM OF CONGENITAL MYOPATHY, A GROUP OF HETEROGENEOUS MUSCLE DISORDERS WHICH ARE THOUGHT TO RESULT FROM ABNORMAL MUSCLE DEVELOPMENT. MUSCLE WEAKNESS IS EITHER NON-PROGRESSIVE OR SLOWLY PROGRESSIVE AND APPARENT FROM BIRTH OR EARLY INFANCY.

CC CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

CC CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC CC

DR AF032108; AAC39708; 1;

DR AF052050; AAC1868; 1;

DR AF072132; AAC80558; 1;

EMBL AJ228836; CAB41534; 1;

FT DISULFID 157 208 BY SIMILARITY.
 FT DISULFID 263 311 BY SIMILARITY.
 FT DISULFID 353 403 BY SIMILARITY.
 FT DISULFID 447 496 BY SIMILARITY.
 FT DISULFID 538 590 BY SIMILARITY.
 FT CARBOHYD 100 100 BY SIMILARITY.
 FT CARBOHYD 202 202 BY SIMILARITY.
 FT CARBOHYD 246 246 BY SIMILARITY.
 FT CARBOHYD 293 293 BY SIMILARITY.
 FT CARBOHYD 432 432 BY SIMILARITY.
 FT CARBOHYD 478 478 BY SIMILARITY.
 FT CARBOHYD 489 489 BY SIMILARITY.
 FT CARBOHYD 504 504 BY SIMILARITY.
 FT CARBOHYD 587 587 BY SIMILARITY.
 FT CARBOHYD 670 670 BY SIMILARITY.
 FT CARBOHYD 725 725 BY SIMILARITY.
 FT CARBOHYD 776 776 BY SIMILARITY.
 FT CARBOHYD 824 824 BY SIMILARITY.
 FT CARBOHYD 848 848 BY SIMILARITY.
 FT CARBOHYD 875 875 BY SIMILARITY.
 FT CARBOHYD 968 968 BY SIMILARITY.
 FT CARBOHYD 1022 1022 BY SIMILARITY.
 FT CARBOHYD 1030 1030 BY SIMILARITY.
 FT CARBOHYD 1073 1073 BY SIMILARITY.
 FT CARBOHYD 1107 1107 BY SIMILARITY.
 SQ 1260 AA: 140968 MW: 22B857001CB2A38 CRC64:
 Query Match 36.1%; Score 45.5%; DB 1; Length 1260;
 Best Local Similarity 61.1%; Pred. No. 53; Mismatches 2;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 OY 2 DQBERGDDNDISPPSGDQ 19
 Db 558 DLQERGDDSD-KYFIEDGK 574

RESULT 10

TS2_MOUSE STANDARD: PRT: 301 AA.

ID TS2_MOUSE STANDARD: PRT: 301 AA.

AC Q8VIG3; Q9DALS; CC
 DT 15-JUN-2002 (Rel. 41, Created) CC
 DT 15-JUN-2002 (Rel. 41, Last sequence update) CC
 DT 15-JUN-2002 (Rel. 41, Last annotation update) CC
 DE Testis-specific gene A2 (Male meiotic metaphase chromosome-associated acidic protein) (Meiochroacidin). CC
 DE GN TS2A2. CC
 OS Mus musculus (Mouse). CC
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. CC
 OC NCBI_TAXID=10090; CC
 RN [1] CC
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION. CC
 RN TISSUE=Testis; CC
 RX MEDLINE=98246622; Pubmed=9578619; CC
 RA Tsuchida J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y., CC
 RA Nishimura Y.; CC
 RT "Molecular cloning and characterization of meiochroacidin (male meiotic metaphase chromosome-associated acidic protein)." Dev. Biol. 197:67-76(1998). CC
 RL Dev. Biol. 197:67-76(1998). CC
 RN SEQUENCE FROM N.A. CC
 RX STRAIN=C57BL/6J; TISSUE=Testis; CC
 RX MEDLINE=21055660; Pubmed=11217851; CC
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., CC
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., CC
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., CC
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., CC
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., CC
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., CC
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Okamoto H., CC
 RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., CC
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., CC

RA Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F., CC
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., CC
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.-F., CC
 RA Lyons P., Marchionni L., Mashima J., Mazzarolli J., Sakamoto N., CC
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sato K., Schenck C., CC
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., CC
 RA Suzuki H., Toyro-oka K., Wang K.-H., Weitz C., Whittaker C., Wilming L., CC
 RA Wynnshaw-Boris A., Yoshida K., Hasagawa Y., Kawai H., Kohtsuki S., CC
 RA Hayashizaki I.; CC
 RA "Functional annotation of a full-length mouse cDNA collection." RL
 CC Nature 409:683-690(2001). CC
 CC -!- FUNCTION: The specific expression during male germ cell development and its characteristic localization suggest that it may play an important role in male meiosis. CC
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic in late spermatocytes, secondary spermatocytes and round spermatids. Gathered around metaphase chromosomes during meiotic divisions. CC
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing. CC
 CC -!- TISSUE SPECIFICITY: Germ cell specific. Specifically expressed in testis, and to a lower extent in ovary. Not expressed in somatic tissues. CC
 CC -!- DEVELOPMENTAL STAGE: During male germ cell development it is not detected until 12 days. Significant expression is detected from 14-day-old through to adult testis. Expression is first detected in the pachytene spermatocytes at stage V, becomes stronger from the late pachytene spermatocytes to round spermatid stage, and then gradually decreases as the morphogenesis proceeds further. Not expressed in germ cells located in the first layer of the seminiferous epithelium (spermatogonia, leptotene and zygotene spermatocytes). CC
 CC -!- SIMILARITY: CONTAINS 6 MORN REPEATS. CC
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 283. CC
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See <http://www.1sb-sib.ch/announce/> or send an email to license@1sb.sib.ch. CC
 CC -----
 DR EMBL: AB006525; BAB83653; 1; ALT_FRAME. DR
 DR EMBL: AK005739; BAB24214; 1; DR
 DR MGDB: MG1.1191909; Tsga2. DR
 DR InterPro: IPR003409; MORN. DR
 DR Pfam: PF02493; MORN; 6. DR
 DR Melo5; Repeat; Alternative splicing. DR
 DR KW -----
 DR DOMAIN 195 201 POLY-GLU. DR
 DR REPEAT 20 43 MORN REPEAT 1. DR
 DR REPEAT 44 66 MORN REPEAT 2. DR
 DR REPEAT 67 89 MORN REPEAT 3. DR
 DR REPEAT 90 112 MORN REPEAT 4. DR
 DR REPEAT 113 135 MORN REPEAT 5. DR
 DR REPEAT 159 181 MORN REPEAT 6. DR
 DR CONFLICT 39 39 P > S (IN REF. 1). DR
 DR SEQUENCE 301 AA: 34181 MW: 704ABERFB94DFC90E CRC64: DR

RESULT 11

TS2_HUMAN STANDARD: PRT: 309 AA.

ID TS2_HUMAN 08WY4; AC
 AC 08WY4; DT 15-JUN-2002 (Rel. 41, Created)

Query Match 35.7%; Score 45; DB 1; Length 301;
 Best Local Similarity 37.5%; Pred. No. 12; Mismatches 6; Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0; OY 2 DQBERGDDNDISPPSGD 17
 Db 8 ELBEEGENDGEVEGE 23

DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Testis specific gene A2 (Male meiotic metaphase chromosome-associated
 DE acidic protein) (Meichoacidin).
 DE TSCA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Futheria; Primates; Catarhini; Homidae; Homo.
 OC OX NEBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98346622; PubMed=9578619;
 RA Tsuchida J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y.,
 RA Nishimura Y.;
 RT "Molecular cloning and characterization of meichoacidin (male meiotic
 RT metaphase chromosome associated acidic protein).";
 RL Dev. Biol. 197:67-76(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Shimizu N., Kudo J., Shibuya K.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 CC -I- FUNCTION: May play an important role in male meiosis. (By
 CC similarity).
 CC -I- SUBCELLULAR LOCATION: Cyttoplasmic in late spermatocytes, secondary
 CC spermatocytes and round spermatids. Gathered around metaphase
 CC -I- TISSUE SPECIFICITY: Testis specific.
 CC -I- SIMILARITY: CONTAINS 6 MORN REPEATS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; S81598; AdB36147.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR00334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
 DR SIGNAL 1
 FT CHAIN 27 393
 FT ACT_SITE 34 34
 FT ACT_SITE 152 152
 FT DOMAIN 270 385
 FT CARBOHYD 343 343
 SQ SEQUENCE 393 AA; 39594 MW; 65C733C610D6A03 C064;
 KW Meiosis; Repeat.
 FT 195 201 POLY-GLU.
 FT DOMAIN 298 301 POLY-GLU.
 FT REPEAT 20 43 MORN REPEAT 1.
 FT REPEAT 44 66 MORN REPEAT 2.
 FT REPEAT 67 89 MORN REPEAT 3.
 FT REPEAT 90 112 MORN REPEAT 4.
 FT REPEAT 113 135 MORN REPEAT 5.
 FT REPEAT 159 181 MORN REPEAT 6.
 SQ SEQUENCE 309 AA; 35124 MW; 09A20A766D05A6A08 CRC64;
 RESULT 12
 Query Match 35.7%; Score 45; DB 1; Length 393;
 Best Local Similarity 46.7%; Pred. No. 12; Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 DLQERGNDTISPFSS 16
 Db 8 ELEEGENDIGEYEG 22
 RESULT 13
 SNCB_BACAM SACB_BACAM STANDARD; PRT; 472 AA.
 ID SNCB_BACAM AC P21130;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl
 DE transferase) (Sucrose 6-fructosyl transferase).
 DE SACB.
 OS Bacillus amyloliquefaciens
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 AC P54424;
 DT 01-OCT-1996 (Rel. 34, 'Created')
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Endogluconase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)
 DE (Cellulase 1) (EG 1).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RX MEDLINE=91092506; PubMed=2265762;
 RA Tang D.B., Lenesra R., Borchert T.V., Vasanthan N.;
 RT "Isolation and characterization of levansucrase-encoding gene from
 RT Bacillus amyloliquefaciens.";

SQ SEQUENCE 851 AA; 96657 MW; A991F3C7E3D980BE CRC64;
Query Match 35.7%; Score 45; DB 1; Length 851;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 TDLQERGDNDSPEFG 18
Db 382 TNLQDSTDNDISESEBG 399

Search completed: January 17, 2003, 13:18:02
Job time : 11 secs

Result		ALIGNMENTS				SUMMARIES	
No.	Score	Query	Match Length	DB	ID	Description	
1	126	100.0	525	4	Q9NQ76	RESULT 1	
2	123	97.6	500	6	Q95KG5	Q9NQ76	PRELIMINARY; PRT; 525 AA.
3	123	97.6	555	6	Q9GM13	AC	01-OCT-2000 (TRIMBLREL. 15, Created)
4	123	97.6	555	6	Q9NQ76	DT	01-OCT-2000 (TRIMBLREL. 15, Last sequence update)
5	81	64.3	433	11	Q92A11	DR	01-DEC-2001 (TRIMBLREL. 19, Last annotation update)
6	81	64.3	435	11	Q9ES02	DE	MATRIX extracellular phosphoglycoprotein precursor.
7	52	41.3	320	2	Q52676	GN	MEPE.
8	49.5	39.3	793	5	Q9WV00	OS	Homo sapiens (Human).
9	49	38.9	752	4	Q9C091	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
10	48	38.1	277	16	Q8YI83	OX	NCBI_TaxID=9606;
11	48	38.1	385	12	Q92A32	RN	[1]
12	48	38.1	440	2	Q9FSV2	RP	SEQUENCE FROM N. A.
13	48	38.1	484	2	Q44497	RC	TISSUE=BONE;
14	48	38.1	581	5	Q9NK94	RX	MEDLINE=20399567; PubMed=10945470;
15	47	37.3	444	16	Q9KBJ7	RA	Econs M.J., De Zoysa P.A., Dong R., Wang H.R., White K.E.,
16	47	37.3	477	2	Q8RSS1	RT	Rowe P.S.N., Oude C.L.;
						RT	*MEPE, a new gene expressed in bone marrow and tumors causing osteomalacia.;
						RL	Genomics 67:54-68(2000)
						RN	
						RP	SEQUENCE FROM N. A.
						RX	MEDLINE=21309068; PubMed=1414762;
						RA	Argiro L., Desbrats M., Glorieux F.H., Ecarot B.;
						RT	*Mepe, the gene encoding a tumor-secreted protein in oncogenic hypophosphatemic osteomalacia, is expressed in bone.;
						RL	Genomics 74:342-351(2001);
						DR	EMBL: AJ276396; CAB97250; 1;
						EMBL	AF325916; AAK70343; 1;
						DR	
						KW	
						SIGNAL	
						FT	17 POTENTIAL.
						FT	18 525 MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN.
						SEQUENCE	525 AA; 58419 MW; 0977CA6E871CA9E5 CRC64;
						SQ	
						Query Match	100.0% Score 126: DB 4; length 525;
						Best Local Similarity	100.0% Pred. No. 4.4e-11;
						Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Osteoregulin.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBL_Taxid=10116;
 RP SEQUENCE FROM N.A.
 RC STRAINS=SPRAGUE-DALEY;
 RX MEDLINE=2059633; PubMed=10967096;
 RA Petersen, D.N., Tkalcicovic, G.T., Mansolf, A.L., Rivera-Gonzalez, R.,
 RA Brown, T.A.,
 RT "Identification of Osteoblast/Osteocyte Factor 45 (Of45), a Bone-Specific cDNA Encoding an RGD-containing Protein That Is Highly Expressed in Osteoblasts and Osteocytes.";
 RT *J. Biol. Chem.* 275:36172-36180 (2000).
 DR EMBL: AF260922; AASJ3666.1;
 SQ SEQUENCE 435 AA; 46515 MW; D587F02968A26BCB CRC64;

Query Match 64.3%; Score 81; DB 11; Length 435;
 Best Local Similarity 75.0%; Pred. No. 0.00032; DB 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 DQERGNDISPGDQPF 21
 |||||||:|||||||
 Db 165 DQVRGNDVPPFGDQHF 184

RESULT 7
 ID 052676 PRELIMINARY; PRT; 320 AA.
 AC 052676;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBrel. 15, Last annotation update)
 DE Porin.
 GN PORCA.
 OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Rhodobacter.
 OC NCBI_TaxID=1061;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=37B4;
 RX MEDLINE=97149280; PubMed=8996088;
 RT Molecular characterization and organization of porin from Rhodobacter capsulatus strain 37B4.";
 RL Gene 183:61-68(1996).
 DR EMBL: U57653; AAB41301.1; -.
 DR HSSP: P31243; 2POR.
 RA SEQUENCE 320 AA; 33396 MW; B0E1745CB9D86F93 CRC64;

Query Match 41.3%; Score 52; DB 2; Length 320;
 Best Local Similarity 58.8%; Pred. No. 7; Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TDLOERGNDNDISPGSGD 17
 ||||:|||:|||:|||
 Db 112 TDLDRGNDIPYLTG 128

RESULT 8
 ID 09VY0 PRELIMINARY; PRT; 793 AA.
 AC 09VY0;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)
 DR 01-JUN-2000 (TREMBrel. 14, Last annotation update)
 DE CG14085 protein.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephidoidea; Dirosophilidae; Drosophila;
 OC NCBL_TaxID=7227;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams, M.D., Calinier, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,
 RA Adams, D.P., Celinier, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,
 RA Amantacites, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,
 RA George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,
 RA Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,
 RA Brandon, R.C., Rogers, Y.-H.C., Blazquez, R.G., Chang, M., Chen, L.X.,
 RA Wan, K.H., Doyle, C., Baxter, E.G., Heit, G., Nelson, C.R., Miklos, G.L.G.,
 RA Abril, J.F., Agbayani, A., An, H.-J., Andrews, P., Prahmkoch, C., Baldwin, D.,
 RA Ballou, R.M., Basu, A., Baxendale, J., Basile, E.M., Beayrakaroglu, L., Beasley, E.M.,
 RA Besson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S.,
 RA Borkova, D., Botchan, M.R., Bouck, J.J., Brokstein, P., Brottier, P.,
 RA Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I.,
 RA Cherry, J.M., Cowley, S., Dahake, C., Davenport, L.B., Davies, P.,
 RA de Pablo, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,
 RA Dooson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Dunn, P.,
 RA Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W.,
 RA Fosler, C., Gabrieleian, A.E., Garg, H.N.S., Gelbart, W.M., Glässer, K.,
 RA Glodek, A., Gong, F., Gorrell, E., Guo, Z., Guan, P., Harris, M.,
 RA Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J.,
 RA Hostin, D., Houston, K.A., Howland, T.J., Wei, M.-H., Ibegwam, C.,
 RA Jaiwall, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum,
 RA Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z.,
 RA Lasko, P., Lei, J., Levitsky, A.R., Li, J., Li, Z., Liang, Y., Lin, X.,
 RA Liu, X., Mattel, B., McIntosh, T.C., McLeod, M.P., McPherson, D.,
 RA Merkulov, G., Milisina, N.V., Mobarry, C., Morris, J., Moshrefi, A.,
 RA Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L.,
 RA Nelson, D.R., Nelson, K., Nixon, K., Nusskern, D.R., Pacile, J.M.,
 RA Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G.,
 RA Reinert, K., Remington, K., Saunders, R.D.C., Scheeler, F., Shen, H.,
 RA Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T.,
 RA Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E.,
 RA Starks, R., Tector, C., Turner, R., Venter, J.C., Wang, A.H., Wang, X.,
 RA Wang, Z.-Y., Wasserman, D.A., Weinstock, G.M., Weissenbach, J.,
 RA Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A.,
 RA Ye, J., Yeh, R.-F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L.,
 RA Zheng, X.H., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O.,
 RA Gibbs, R.A., Myers, E.W., Rubin, G.M., Venter, J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT *Science* 287:2185-2195(2000).
 DR EMBL: AB003517; AAF49175.1; -.
 DR SEQUENCE 793 AA; 88674 MW; EFC003DF3E537C41 CRC64;
 SQ FlyBase: FBgn0338859; CG144085;
 SQ SEQUENCE 793 AA; 88674 MW; EFC003DF3E537C41 CRC64;

RESULT 9
 ID 09C091 PRELIMINARY; PRT; 752 AA.
 AC 09C091;
 DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE KIAA1772 protein (Fragment).
 GN KIAA1772 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBL_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:21083932; PubMed=11214970;
 RA Nadass T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes. XIX.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro.";
 RL DNA Res. 7:347-355 (2000).
 DR EMBL: AB051159; BAB21063.1; -;
 DR InterPro: IPR001669; ASPROTEASE_SITE.
 DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 752 AA; 82489 MW; 7BEA604AA823D2E4 CRC64;
 Query Match 38.9%; Score 49; DB 4; Length 752;
 Best Local Similarity 57.1%; Pred. No. 55;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 QERGDNNDSPFSGD 17
 Db 630 QRGGDSVVPFBD 643

RESULT 10
 QBY183 PRELIMINARY; PRM; 277 AA.
 ID QBY183;
 AC QBY183;
 DT 01-MAR-2002 (TREMBREL 20, Created)
 DT 01-MAR-2002 (TREMBREL 20, Last sequence update)
 DE Lysozyme M1 precursor (EC 3.2.1.17).
 GN BME10562.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 QX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-T3;
 RC Maeda S.;
 RA Maeda S.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T3;
 RA Gomi S.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L33180; AAC63740.1;
 SQ SEQUENCE 385 AA; 44875 MW; 1B2F1A12EB8207BB CRC64;
 Query Match 38.1%; Score 48; DB 12; Length 385;
 Best Local Similarity 56.2%; Pred. No. 36;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Qy 8 DNDIDISPFGDGPFKD 23
 ID QDF5V2
 AC QDF5V2;
 PRM; 440 AA.
 DT 01-MAR-2001 (TREMBREL 16, Created)
 DT 01-MAR-2001 (TREMBREL 16, Last sequence update)
 DR 01-JUN-2002 (TREMBREL 21, Last annotation update).
 DE RteB.
 GN RteB.
 OC Bacteroides fragilis.
 OC Bacteroides; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
 OC Bacteroides.
 QX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPONSON-CTN25585;
 RA Smith C.J.; Bayley D.;
 RT "The putative IS1224 insertion sequence is actually part of a large
 genetic element with similarity to the Bacteroides conjugative
 transposons.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
 DOMAIN.
 DR EMBL: AF30352; AAC17462.1; -;
 DR InterPro: IPR00593; AAA_AMPase.
 DR InterPro: IPR00197; HTH_FIS.
 DR InterPro: IPR00789; Response_reg.
 DR InterPro: IPR002078; Sig54_interact.
 PFam: PF02054; RPH_8_1.
 PFam: PF00072; response_reg; 1.

RESULT 11
 Q92432 PRELIMINARY; PRM; 385 AA.
 ID Q92432;
 AC Q92432;
 DT 01-NOV-1998 (TREMBREL 08, Created)
 DT 01-NOV-1998 (TREMBREL 08, Last sequence update)
 DT 01-DEC-2001 (TREMBREL 19, Last annotation update)
 DE LBF_3ACMNPV orf67.
 GN DRF-3.

DR	Pfam; PRO0158; SIGMAM54_activat; 1.	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
DR	PRINTS; PR01590; HTHFIS.	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
DR	PRODOM; PD000039; Response_reg; 1.	OC	Ephydrioidea; Drosophilidae; Drosophila.
DR	SMART; SW00302; AAA; 1.	OX	NCBI_TAXID=7227;
DR	SMART; SW00448; RBC; 1.	RN	RN
DR	TIGRFAMS; TIGR01199; HTH_fis; 1.	RP	[1]
DR	PROSITE; PS00676; SIGMAM54_INTEGRCT_2; 1.	RC	SEQUENCE FROM N.A.
DR	PROSITE; PS50045; SIGMAM54_INTERACT_4; 1.	RC	STRAIN=BERKELEY;
DR	ATP-binding; DNA-binding; Phosphorylation; Sensory transduction;	RC	MEDLINE=99403001; PubMed=10471707;
KW	transcription regulation.	RA	Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Gallo R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnston G., Martin C., Mosheri A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
KW	SEQUENCE 440 AA; 49627 MW; 611F28F8A91E0799 CRC64;	RA	"An exploration of the sequence of a 2.9-Mb region of the genome of
Query	Query Match 38.1%; Score 48; DB 2; Length 440; Best Local Similarity 52.0%; Pred. No. 42; Matches 13; Conservative 2; Mismatches 8; Indels 2; Gaps 1;	RT	Drosophila melanogaster; the Adh region.";
Db	QY 1 TDQER-GDNDISPPFGQPKD 23 118 TILKERNIGRNRMVFSRDGSAFKD 142	RT	RL
RESULT 13	SEQUENCE FROM N.A.	RN	[2]
ID	Q44497 PRELIMINARY; PRT; 484 AA.	RP	SEQUENCE FROM N.A.
AC	Q44497; P94201;	RC	STRAIN=BERKELEY;
DT	01-NOV-1996 (TREMBLrel. 01, Created)	RA	Celniker S.E., Agbayani A., Arcalina T.T., Baxter E., Blazej R.G., Butenhoff C., Champre M., Chavez C., Chew M., Ciesiolkia L., Doyle C.M., Farfan D.E., Gallo R., George R.A., Harris N.L., Hoskins R.A., Houston K.A., Hummasti S.R., Karrha K., Kearney L., Kim E., Lee B., Lewis S., Li P., Lomotan M.A., Mazda P., Mosheri A.R., Mosheri A., Nixon K., Pacleb J.M., Park M., Pfeiffer B., Poon L., Sequeira A., Sethi H., Snir E., Svirskas R.R., Wan H.H., Weinburg T., Zhang R., Zierman L.L., Rubin G.M., Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	DR	EMBL; AE003112; ARF4927; 1; -
DE	ALGJ protein.	DR	ENSEMBL; FBgn0028861; BG; DS07295.4.
GN	ALGJ.	DR	FLYBase; FBgn0028861; BG; DS07295.4.
OS	Autobacter vinelandii.	DR	HYPOBASE; FBgn0028861; BG; DS07295.4.
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	DR	SEQUENCE 581 AA; 64222 MW; 44841FDF16526701 CRC64;
OC	Autobacter; Proteobacteria; Pseudomonadaceae;	DR	Best Local Similarity 47.1%; Pred. No. 58; Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OX	NCBI_TAXID=354;	Db	QY 7 GONDISPPSGDGPKD 23 405 GANNLSPIPATEHPVKD 421
RN	SEQUENCE FROM N.A.	DR	Query Match 38.1%; Score 48; DB 5; Length 581; Best Local Similarity 47.1%; Pred. No. 58; Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
RP	[2]	DR	RT
RC	STRAIN=E;	DR	RT
RX	MEDLINE=97090405; PubMed=8936313;	DR	RT
RA	Rehm B. H.A.;	DR	RT
RT	"The Autobacter vinelandii gene algJ encodes an outer-membrane protein presumably involved in export of alginate.";	DR	RT
RL	Microbiology 12:87-88(1996).	DR	RT
RN	[2]	DR	RT
RP	SEQUENCE FROM N.A.	DR	RT
RC	STRAIN=E;	DR	RT
RX	MEDLINE=97090405; PubMed=8936313;	DR	RT
RA	Rehm B. H.A.;	DR	RT
RT	"The Autobacter vinelandii gene algJ encodes an outer-membrane protein presumably involved in export of alginate.";	DR	RT
RL	Microbiology 12:87-88(1996).	DR	RT
RN	[2]	DR	RT
RP	SEQUENCE OF 1-128 FROM N.A.	DR	RT
RC	STRAIN=ATCC9041-6;	DR	RT
RX	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.	DR	RT
RA	Mejia Ruiz H., Moreno S., Guzman J., Najera R., Soberon-Chavez G., Espin G.;	DR	RT
RA	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.	DR	RT
RA	EMBL; X85333; CA60245.1; -.	DR	RT
DR	EMBL; X98833; CA67371.1; -.	DR	RT
DR	InterPro; IPR002106; ATRNA_ligaseII.	DR	RT
DR	PROSITE; PS00119; ATRNA_LIGASE_II_1; UNKNOWN_1.	DR	RT
SQ	SEQUENCE . 484 AA; 54611 MW; 0A4CCF18C928DBD3; CQC64;	DR	RT
Query	Query Match 38.1%; Score 48; DB 2; Length 484; Best Local Similarity 47.4%; Pred. No. 47; Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;	DR	RT
Db	QY 2 DLQERODNDISPPFGQGP 20 393 DDEDLGQNGISPPIEKGK 411	DR	RT
RESULT 14	SEQUENCE FROM N.A.	DR	RT
ID	Q9NK94 PRELIMINARY; PRT; 581 AA.	DR	RT
AC	Q9NK94; P94200 (TREMBLrel. 15, Created)	DR	RT
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DR	RT
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DR	RT
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DR	RT
DE	Hypothetical 64.2 kDa protein.	DR	RT
DE	NCBI_TAXID=86665;	DR	RT
OS	Drosophila melanogaster (Fruit fly).	DR	RT

DR PROSITE: PS00137: SUBTILASE_HIS; 1.
DR PROSITE: PS00138: SUBTILASE_SER; 1.
KW Protease; Complete proteome.
SQ SEQUENCE 444 AA; 48916 MW; 3B05FB1C53A21F2F CRC64;
Query Match Similarity 37.3%; Score 47; DB 16; Length 444;
Best Local Similarity 47.1%; Pred. No. 61;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 2 DIQERGNDISPGDG 18
| : : | : : || |
Db 319 DRDREDDDVAPFSSRG 335

Search completed: January 17, 2003, 13:18:38
Job time : 30 secs